

**FIGURE 1**

CCAATGCCCGGTGCGGTGGTGCAGGGCTCGGGCTAGTC**ATG**GCCTCCCGTCTCGGAGAC  
TGCAGACTAAACCAGTCATTACTTGTTCAGAGCGTTCTGCTAATCTACACTTTATTTTC  
TGGATCACTGGCGTTATCCTTCTGCAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA  
CTTTCTCTTTAAATGAGAAGGCCACCAATGTCCCCTCGTGCTCATTGCTACTGGTACCG  
TCATTATTCTTGGCACCTTGGTTGTTGCTACCTGCCAGCTCTGCATGGATGCTA  
AAACTGTATGCAATGTTCTGACTCTCGTTGGTCGAACGGTCGCTGCCATCGTAGG  
ATTTGTTTCAGACATGAGATTAAGAACAGCTTAAGAATAATTATGAGAAGGCTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAACGCATGCAGTAGACAAGATCCAAAATACGTTGCAT  
TGTTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
TCCTAACAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTCCTTGGAGTTGCTTCCAAGTGGATCTGGAAATCTTCTCGCCTACTGCCWCTCTCG  
TGCCATAACAAATAACCAGTATGAGATAGTGT**TAA**CCCAATGTATCTGTGGGCCTATTCTCT  
CTACCTTAAGGACATTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG  
ACAACACTACTGATAGACCAAAAAACTACACCAAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGCTGAT  
TCAATCAAGATGTATGTTGCTATGTTCTAAGTCCACCTCTATCCCATTGTTAGATCG  
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGAAATGAAGT

## **FIGURE 2**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLNEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

**N-glycosylation site.**

amino acids 134-138

**Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

**N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

### **FIGURE 3**

## **FIGURE 4**

MIVFGWAVFLASRSLGQGLLTLEEHIAHFLGTGGAATTMGNSCI  
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKQNVDGLVLDTLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

**FIGURE 5**

GGCACGAGGCCTGTCCACCCGGGGCGTGGGAGTGAGGTACCA  
GGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTAACGGACTG  
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGCATGCAAATGTGGGTGACCTCGTCTCAGGCTTCCTGCTTCCGAAGC  
CTTCCCCGACATACTCGGACTAGTGCAGAGCAAACCTTCCCCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTACCTGCTGTTCTGAGCCTACGCTGGCCACTGTCAAC  
GCCCGCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGTGGGAGGTACCAAGGCAGCCACCAGGGTCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGCTCCGCCAGAATTCTTCCGCTACCATGGGCTGTCC  
TCTCTTGCAATCTGGGCTGCGCCTGAGCAATGGGCTCTGTCTCGCTGGCCTGCCCTGGA  
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAATGCTTCTCAGAAATGAAAAAAA  
AAAAAAAAAAA

## **FIGURE 6**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107
<subunit 1 of 1, 231 aa, 1 stop
<NX(S/T): 0
MEEGGNLGGLIK MVHLLVLSGA WGMQM WVT FVSGFLLFRSL PRHT FGLVQSKLFPFYFHISM
GCAF INLCILASQHAWAQLTFWEASQLYLLFLSLT LATVNARWLEPRTTAAMWALQTV EKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGL ALEIRSL
```

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

## FIGURE 7

AATTCA GATT TAAG CCCATTCTGCAGT GGAATT CATGA ACTAGCAAGAGGACACCATCTT  
 CTTGTATTATA CAAGAAAGGAGTGTACCTATCACACAGGGGGAAAA **ATG**CTCTTTGGGT  
 GCTAGGCCTCCTAATCCTCTGGTTCTGTGGACTCGTAAAGGAAACTAAAGATTGAAG  
 ACATCACTGATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGGAAACTTGGCAGCC  
 AGAACTTTGATAAAAAGGGATTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
 AGCTTAAAGGCAGAACCTCAGAGAGACTCGTACTGTGCTCTGGATGTGACCGACCCAG  
 AGAATGTCAAGAGGACTGCCAGGGTGAAGAACCAAGTTGGGAGAAAGGTCTGGGT  
 CTGATCAATAATGCTGGTGTCCCGCGTGCTGGCTCCACTGACTGGCTGACACTAGAGGA  
 CTACAGAGAACCTATTGAAGTGAACCTGTTGGACTCATCAGTGTGACACTAAATATGCTTC  
 CTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAAATGTCTCCAGTGGAGGTCGCCTTGCA  
 ATCGTTGGAGGGGGCTATACTCCATCAAATATGCAGT GGAAGGTTCAATGACAGCTTAAG  
 ACGGGACATGAAAGCTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA  
 ACTTGGCAGATCCAGTAAAGGTAAATTGAAAAAAACTGCCATTGGGAGCAGCTGTCTCCA  
 GACATCAAACAACAATATGGAGAAGGTTACATTGAAAAAAAGTCTAGACAAACTGAAAGGCAA  
 TAAATCCTATGTGAACATGGACCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA  
 GTCTCTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAATTTCTGGATACCTCTG  
 TCTCACATGCCAGCAGCTT GCAAGACTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
 TCCCAAGGCAGTGT**TGA**CTCAGCTAACCAACAAATGTCTCCAGGCTATGAAATTGCCGAT  
 TTCAAGAACACATCTCCTTTCAACCCATTCTTATCTGCTCCAACCTGGACTCATTAGA  
 TCGTGCTTATTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCAGGGTCCCTG  
 CTCAAGTTCTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT  
 ATTTAGGCTTGCCTGCTGGTGTGATGTAAGGAAATTGAAAGACTTGCCATTCAAATG  
 ATCTTACCGTGGCCTGCCCATGCTTATGGTCCCAGCATTACAGTAACCTGTGAATGTT  
 AAGTATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAA  
 AAAAAAAA

## **FIGURE 8**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT
ESGSTALKAETSERLRTVLLDVTDPEVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGlisVTLNMLPLVKKAQGRVINSSVGGRЛАIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEFYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

## FIGURE 9

GCAGGGCTGTTGACGGCGCTGCG**ATGG**CTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
 CCTCTCAGTCGGACTTCCCTGACGCCGAGTGGCGGGGCCCTTGGCGCTGCCACCACT  
 GTAGTCATGTACCCACCGCCGCCGCCTCATCGGACTTCATCTCGGTGACGCTGAG  
 CTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCCGCTCGTGTGGAGGAAATGGA  
 AGCAACTGTGAGATTGAGCGGAATATGATTCTCTCCTGCCTTCTGCTTTCTGT  
 GGACTCCTCTTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTCAGGCTAGAGGA  
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTTAAACCAGCAAATCCACCCGTCTTACCA  
 CTCCTCAGAAGGCCGACACCGACCCCTGAGAACTTACCTGAGATTTCGTACAGAAGACACAA  
 AGACACATCCAGCAGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA  
 TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAAGGCCCTGTGGATCCCCGCCGAAGGAG  
 ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG  
 CTCCCTCAAGAAGAGCAGAAGTGCCTCCACAGCCTCCCTGCCACCGCCAGGACACAGGG  
 CACACCAGTCATCTGAACTATGCCAGAAGGGCGTGATTGACGTCTCCTGCATGCATGGA  
 AAGGATAACCGCAAGTTGCATGGGCCATGACGAGCTGAAGCCTGTCAGGTCTTCAGT  
 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACCGCGTGGACACCATGTGGATCTGGGTCT  
 GAGGAAAGAATTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTGAAAAGGACG  
 TGGACGTCAACCTGTTGAGAGCACGATCCGCATCCTGGGGGGCTCTGAGTGCCTACCAC  
 CTGCTGGGGACAGCCTCTCCTGAGGAAAGCTGAGGATTGGAAATCGGTAATGCCTGC  
 CTTCAGAACACCATCCAAGATTCTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC  
 CGCCACGGTGGACCTCCGACAGCACTGTGGCGAGGTGACCAGCATTAGCTGGAGTCCGG  
 GAGCTCTCCGTCTCACAGGGATAAGAAGTTCAGGAGGCAGTGGAGAAGGTGACACAGCA  
 CATCCACGGCCTGTCTGGGAAGAAGGTGGCTGGTGCCTATGTCATCAATACCCACAGTG  
 GCCTCTCACCCACCTGGCGTATTACGCTGGCGCAGGGCGACAGCTACTATGAGTAC  
 CTGCTGAAGCAGTGGATCCAGGGCGGAAGCAGGAGACACAGCTGTTGGAAGACTACGTGGA  
 AGCCATCGAGGGTGTCAAGACGCACCTGCTGCGGCACTCCGAGGCCAGTAAGCTCACCTTG  
 TGGGGAGCTGCCACGGCGCTTCAGTGCAAGATGGACCACCTGGTGTGCTTCTGCCA  
 GGGACGCTGGCTCTGGCGTCTACCACGGCTGCCAGCCACATGGAGCTGGCCAGGA  
 GCTCATGGAGACTTGTACCAAGATGAACCGGCAGATGGAGACGGGCTGAGTCCCAGATCG  
 TGCACCTCAACCTTACCCCCAGCCGGCGTGGGACGTGGAGGTCAGGCCAGCAGACAGG  
 CACAACCTGCTGCGGCCAGAGACCCTGGAGAGCCTGTTACCTGTACCGCGTCACAGGGGA  
 CCGCAAATACCAAGGACTGGGCTGGGAGATTCTGAGAGCTTCAGCCGATTACACGGTCC  
 CCTCGGGTGGCTATTCTCATCAACAATGTCCAGGATCCTCAGAAGCCCAGCCTAGGGAC  
 AAGATGGAGAGCTTCTCCTGGGGAGACGCTCAAGTATCTGTTCTGCTCTCCGATGA  
 CCCAAACCTGCTCAGCCTGGACGCCACGTGTTCAACACCGAAGCCCACCCCTGCTCATCT  
 GGACCCCTGCC**TAG**GGTGGATGGCTGGTGTGGGACTTCGGTGGCAGAGGCACCTTG  
 CTGGGTCTGGCATTTCAGGGCCACGTAGCACCAGCAACGGCAAGTGGCCAGGCT  
 CTGAACACTGGCTCTGGCTCCTCCTCGTCTGCTTAACTCAGGACACCCTGAGGACAAGTGA  
 GGCGTCAGTCTGGTGTGATGCGGGTGGGCTGGCGCTGGAGGCTCCGCTGCTCCTC  
 CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCAGCA  
 GAGGGGGCTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCCAGGGTGCAGC  
 TCTGCCGGGCTCGTAAGCCTCAGATGTCCCCAATCCAAGGGTCTGGAGGGCTGCCGTGA  
 CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTGTTACAAGCTGGACTCAGGGATCCTC  
 CTGGCCGCCCGCAGGGGGCTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGCCCT  
 CCAGTGGAAATGGGTCTTTCGGTGGAGATAAAAGTTGATTGCTTAACCGCAA

## **FIGURE 10**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTPVGGAPWAVATTVVMPPPPPPHRDFISVTLSFGESYDN
SKSWRRRSCWRWKQLSRLQRNMILFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLK PANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPREGPDPQRTVISWRGAVIEPEQGTTEPSRRAEVPTKPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTL GARADSYYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLT FVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNL RPETVESLFYLYRTGDRKYQDWG
WEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

## FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGCCGGCCGGCTGCGAGCGCCTGCCCATGCGCCGC  
 CGCCTCTCCGCACG**ATG**TTCCCTCGCGAGGAAAGCGCCGAGCTGCCCTGGAGGACGGC  
 AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCGTCTCCACCTGTTCGTGGC  
 CTGCCTCTCGCTGGGCTTCTTCTCCACTCTGGCTGCAGCTCAGCTGCTCTGGGACGTGG  
 CCCGGCAGTCAGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCAGAG  
 CCGCCCCCTGAGCACTGGAAAGAAGACGCATCCTGGGCCCCACCGCCTGGCAGTGCTGGT  
 GCCCTTCCCGAACGCTTCGAGGAGCTCCTGGTCTCGTCCCCACATGCGCCGTTCTGA  
 GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTAAC  
 CGGGCAGCGCTCATAACGTGGGCTTCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTCCTGAGGCTGGC  
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCCTCTTACCACTACAAGACCTATGTCGGCGC  
 ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTCAATGGATGTCCAACCGCTTCTGGG  
 CTGGGCCGAGGACGACGAGTTCTACCGCGCATTAAGGGAGCTGGCTCCAGCTTCC  
 GCCCCTCGGAATCACAACGGTACAAGACATTGCCACCTGCATGACCCAGCCTGGCG  
 AAGAGGGACCAGAAGCGCATCGCAGCTAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
 AGGCCTGAACACTGTGAAGTACCATGTGGCTCCCGACTGCCCTGTCTGGGGCGGGCCC  
 CCTGCACTGTCCCTCAACATCATGTTGGACTGTGACAAGACGCCACACCCGGTGCACATT  
 AGC**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATTGCTCAGGCTCAGGA  
 CAAGGCCTCAGGTCGTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
 AGCTACGCAATTGCAGCCACCCGGCCAGGCTGGCTGGCCAGGACACGTGG  
 GTGCCTGGGACGCTGCTGCCATGCACAGTGATCAGAGAGAGGCTGGGTGTGCTGTCCG  
 GGACCCCCCTGCCTTCTGCTCACCTACTCTGACCTCCTCACGTGCCAGGCCTGTGG  
 TAGTGGGAGGGCTAACAGGACAACCTCTCATCACCTACTCTGACCTCCTCACGTGCC  
 AGGCCTGTGGTAGTGGGAGGGCTAACAGGACAACCTCTCATCACCCCCAAAAAAA  
 AAAAAA

## **FIGURE 12**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVR
GQGQETSGPPRACPPEPPPEHWEEDASWGPRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWRGREDDEFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCKTATPWCTFS
```

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

**FIGURE 13**

CAATGTTGCCTATCCACCTCCCCAAGCCCCCTTACCTATGCTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTAAAGGCTCATGCTTGGAGTGGGACTGGTCGGTGCAGAAAGTCT  
CTTCTGCCACTGACGCCCATCAGGGATTGGGCCTCTTCCCCCTCCTTCTGTGTCTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGT  
GGGGATGGCTAAGAAAGCTGGGAGATAGGAACAGAACAGGGTAGTGGGTGGCTAGGGGG  
GCTGCCTTATTAAAGTGGTTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC  
CCTGTTCAATTAAAGAAATTGTTCCCTCCCTGTGTTCAATGTTGAAAGATTGTTCTGTGT  
AAATATGTCTTATAAACAGTTAAAGCTGAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 14**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862
<subunit 1 of 1, 73 aa, 1 stop
<MW: 7879, pI: 7.21, NX(S/T): 0
MLLLTLLLLLKLGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQ
PRGEGEKVGDG
```

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

## FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGCAGCGGACAAAG  
 GAGCATGTCCCGCCGGGAAGGCCCGTCCCTCCGGCCATAAGGCTCCGGTCGCCGCTGG  
 GCCCGCCGCCGCTCCTGCCCGCCGGCTCCGGGCCGCTAGGCCAGTGCGCCGCG  
 CTCGCCCCGCAGGCCCGGCCGAGC**ATG**GAGCCACCCGGACGCCGGCGGGCCGCGCA  
 GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGGCG  
 GCAGGCCGGCGCCGGCGCTGCCCGCCGGCTGCAAGCACGATGGGCCGGCCCCGAGGGCTGGC  
 AGGGCGGCCGGCGCCGGCAAGGTGGTGCAGCAGCTGGAACCTCGCAGGTCT  
 GCCCCCAGATACTCTGCCCAACCGCACGGTACCCCTGATTCTGAGTAACAATAAGATATCCG  
 AGCTGAAGAATGGCTCATTTCTGGGTTAAGTCTCCTGAAAGATTGGACCTCCGAAACAAT  
 CTTATTAGTAGTATAGATCCAGGTGCCTCTGGGACTGTCATCTCTAAAAGATTGGATCT  
 GACAAACAATCGAATAGGATGTCGAATGCAGACATATTCGAGGACTACCAATCTGGTTC  
 GGCTAAACCTTCGGGAATTGTTCTCATTATCTCAAGGAACCTTGATTATCTGCG  
 TCATTACGGTCTTGGAAATTCCAGACTGAGTATCTTGTTGACTGTAACATACTGTGGAT  
 GCATCGCTGGTAAAGGAGAAGAACATACGGTACGGGATACCGAGTGTGTTATCCTAAGT  
 CACTGCAGGCCAACCAACAGTCACAGCGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT  
 GAATTGCCGTCTTCTACATGACTCCATCTCATGCCAAGTTGTGTTGAAGGAGACAGCCT  
 TCCTTCCAGTGCATGGCTCATATATTGATCAGGACATGCAAGTGTGTTGATCAGGATG  
 GGAGAAATAGTTGAAACCGATGAATCGCAAGGTATTTGTTGAAAAGAACATGATTACAAC  
 TGCTCCTGATTGCAAGTGCCTAACCATTTCTAATATTGAGGCTGGATCTACTGGAAATTG  
 GGGCTGTCACTGCCAGACCAAACGTGGGATAATACGAGGACTGTGGATATTGTTGATTAG  
 AGAGTTCTGCACAGTACTGCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG  
 CCCAGAACATTGGCAGGCATTACTGCATATCTGAGTGTACCGGGAACACCCATGGCAGTGG  
 GATATATCCGGAAACCCACAGGATGAGAGAAAGCTTGGCGCAGATGTGATAGAGGTGGCT  
 TTTGGCAGATGATGATTATTCTGCTGTCAGTATGCAAATGATGTCAGTCACTAGAGTTCTTAT  
 ATGTTAACATCAGATGCCCTCAATCTAACATGCGTGGCAACAGCTGACAGTTACTGGC  
 TTACACTGTGGAAGCAGCCAACCTTCTGACAAAATGGATGTTATATTGTTGAGAACATGA  
 TTGAAAAATTGGAAGATTACCAAGGAGGAAAATCAAAGAGCTAGGTGACGTGATGGTT  
 GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCCTGGCTGGCGCAGAGGGAAGC  
 TAAAGCCTGCAGTAGGATTGTCAGTGTCTCAGCGCATTGCTACCTACCGGCTAGCCGGTG  
 GAGCTCACGTTATTCAACATATTACCCAATTGCTCTGGAAGCTTATGTCATCAAGTCT  
 ACTGGCTCACGGGGATGACCTGTACCGTGTCCAGAAAGTGGCAGCCTCTGATCGTACAGG  
 ACTTCGGATTATGGGAGGCAGGATCCAGAGGAAACCTGGATAAGCAGCTGAGCTTAAAGT  
 GCAATGTTCAAATACATTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCTT  
 AAGACTATTACAGT**TAA**ATTAGAATGCTCAAATGTTGCTTCGAAAATAACCTTATTAA  
 AAAGATTTTTTGCAAGGAAGATAGGTATTATGCTTTGCTACTGTTAAAGAAAAC  
 ACCAGGAAGAACCTGCATTACGACTTCAAGGCCCTAGGCATTTGCTTGTGATTCCCTT  
 CTTCACATAAAATACAGAAATTACATTAACTGCACTGGTATAAATGCAAATATACT  
 ATTGTTACATGTAAGAAAATTGACTTAAAGTTATTGTTATTGTTAAAGTATTGCTCCT  
 GATTTAAGACAATAAGATGTTCATGGGCCCTAAAGTATCATGAGCCTTGGCACTGC  
 GCCTGCCAAGCCTAGTGGAGAAGTCAACCCCTGAGACCAGGTGTTAATCAAGCAAGCTGTAT  
 ATCAAAATTGGCAGAAAACACAAATATGTCATATCTTTTAAAGTATTCA  
 TTGAAGCAAGCAAATGAAAGCATTGTTACTGATTAAAATTGGTGCTTAGATATATT  
 GACTACACTGTATTGAAAGCAAATAGAGGAGGCACAACCTCCAGCACCTAATGGAACCACATT  
 TTTTCACTTAGCTGCTGGCATGTGTAATTGTTCTGCGGTTTAATCTCACAG  
 TACTTTATTCTGTCCTGCTCAATAATATCACAAACAAATTCCAGTCATTAAATGGC  
 TGCATAATAACTGATCCAACAGGTGTTAGGTGTTAGTGTGAGCACTCAATAAATA  
 TTGAATGAATGAACGAAAAA

## FIGURE 16

MEPPGRRRGRAQPPLLPLSLLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
VVCSSLELAQVLPPDTLPNRTVTLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA  
FWGLSSLKRDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT  
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTKQELLTCDPPELPSFYMTP  
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT  
ISNIQAGSTGNWGCHVQTKRGNNRTVDIVVLESSAQYCPPERVNNKGDFRWPRTLAGITA  
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPNL  
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA  
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT  
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
433-437, 453-457, 592-596

**N-myristoylation site.**

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
384-390, 403-409, 554-560

**FIGURE 17**

GCCTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGCCTGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCACAGAGGCTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCACAAATTGGAAAAAGAAAACATTGCTTTGGGAGAACAGATTA  
TTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAA  
**TCA****TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTGTGTGTGTTGAT  
GGAGAGTAGCTTAGTATCTTCATCTTTGGTCACTGTCCTTAAACTGATCA  
AATAAAGGACAGTGGGTATATAAGTTACTGCTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTGGAAGAGTCTGTCGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACAC  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

## **FIGURE 18**

MSRSSKVVLGLSVLLTAATVAGVHVKKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21

## **FIGURE 19**

CTGTCGCTTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCAAGTGTGGCTTAATCCGTCTCCACCACCAAGATCTTCTCCGTGGATTCCCTCTGCTAAGACC  
GCTGCC**ATG**CCAGTGACGGTAACCCGCACCACCATCACAAACCACCGACGTATCTTCGGG  
CCTGGGGTCCCCATGATCGTGGGTCCCCTGGGCCCTGACACAGCCCCTGGTCTCCTCGC  
CTGCTGCAGCTGGTGTACCTCGCTGGCCTCTCGCTGGTGGCTAGCGTGGCGCTGGAC  
GGGGTCCATGGGCAACTGGTCCATGTTCACCTGGTGGCTCTGCTTCTCCGTGACCCTGATCA  
TCCTCATCGTGGAGCTGTGCAGGCTCCAGGCCGCTTCCCTGTCTGGCGCAACTTCCCC  
ATCACCTCGCCTGCTATGCCCTCTTCTGCCTCTGCCCTCCATCATCACCCCCACAC  
CTATGTCCAGTCCCTGTCCCACGCCGTTCGCGGGACCACGCCATGCCGCCACCTTCTTCT  
CCTGCATCGCGTGTGGCTTACGCCACCGAAGTGGCTGGACCCGGGCCGGCGAG  
ATCACTGGCTATATGCCACCGTACCCGGCTGCTGAAGGTGCTGGAGACCTCGTGCCTG  
CATCATCTTCGCGTTCATCAGCGACCCAAACCTGTACCAAGCACCAGCCGGCCCTGGAGTG  
GCGTGGCGGTGACGCCATCTGCTTACCTAGCGGCATGCCATCCTGCTGAACCTGGGG  
GAGTGCACCAACGTGCTACCCATCCCCTCCCCAGCTTCTGTCGGGCTGGCTTGCTGTC  
TGTCCCTCTATGCCACCGCCCTGTTCTCTGGCCCTCTACAGTTGATGAGAAGTATG  
GCCGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCACTACGTGT  
GCCGGACCGCCACTGGCTGTGGCATCCTGACGGCCATCAACCTACTGGGTATGTGG  
TGACCTGGTGCACTCTGCCACCTGGTTTGTCAGGTC**TAA**ACTCTCCAAGAGGCTCC  
CGTCCCTCTCCAACCTCTTGTCTTCTGCCAGTTCTTATGGAGTACTTCTTCC  
TCCGCCCTTCCCTGTTCTCTTCTCTGTCTCCCTGCCCTCCACCTTTCTTCC  
CAATTCTTGCACTCTAACCAAGTCTGGATGCATCTCTTCCCTCCCTTGT  
TTCCTCCTGTGTTGGTACATCCTGTTCAAGGTC**TAA**ACTCTCCAAGAGGCTCC  
CTTTCTTCTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG  
TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCCTGGTTCAAGCGATTCTC  
CCCAGCCTCCAAAGTAGCTGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTCT  
TTCCACTCTCTTCTCATCTCTTCTGGTGCCTGCGCTTCTTATCTGCCTGT  
TTGCAAGCACCTCTCTGTGTCCTGGAGGCCCTGAGACTCTTCTCCTGCC  
CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTGCAAGCGTCCATGCC  
CCAAGGGGCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTAGTCAGTGT  
GTGTGTGTGTGTGTTGGGGGTGGGGTAGCTGGGATTGGCCCTTCT  
CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCTTAAATTAAAAACATATATATAT  
ATTGGAGGTCACTTCCAATGGCGGGAGGCATTAAGCACCACCCCTGGCTTCT  
CCCCGCCTGGCACTCAGCCTGCCAGAGATTGGCTCCAGAATTGGCCAGGCTACAGAACAC  
CCACTGCCTAGAGGCCATCTAAAGGAAGCAGGGCTGGATGCCTTCACTCCAACTATTCT  
CTGTGGTATGAAAAAG

## **FIGURE 20**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTSSSGLSPMIVGSPRALTQPLGLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALEWCVAVYAIKFILAAIAILLNLGECTNVLPPIPFPSSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFKV
```

**Important features:**

**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21

## FIGURE 21

GAACGTGCCACCATGCCAGCTAATTTGTATTTAGTAGAGACGGGTTTACCATGTTGCCAGGCTGGTC  
 TTGAACCTGTGACCTCATGATCGCTCACCTCGGCCCTCCAAAGTGTGGATTACAGGCATGCCACTGACGC  
 CTGCCAGCCTATGCATTAAAGAAATTATTCTGTATTAGGTGCTGTGCTAAACATTGGCACTACAGTACCA  
 AAACAGACTGAATTCCCAAGAGCAAAGACCAGTGAGGGAGACCAACAAGAAACAGGAAATGCAAAAGAGACCA  
 TTATTACTCACTATGACTAAGGGTACAAATGGGTACGTTGATGGAGAGTGATTGTTAAGAGACTACAGAGGG  
 AGGACAGACTACCAAGAGGGGGCAGGAAAGCTCTGACGAGGTGGTATTCAAGCCAAACTGGAAGAATGA  
 GAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGAGCACTACACTCACTACACTTGGCCTGAGAA  
 AATAGCATGGGATTGGAGGAGGCTGGGGAACACCACTCTGCCGACCTGGGCAGGGCAGGGCATTGAGGCCTTGAGA  
 AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTGCAAGGTGGAATCATTAGGTCTTATC  
 AACAGATATGGGCAAGCAAAGCCAGGGAGAATTGATGTTAATGCTGAGGTTGGAGCCAGGCTAGATGGGACAG  
 TGGTGGGTGATGCAAAGGAAAGAGGTCAAGGAAGCAGGGCAGACGTGGGAGAAGGTGTTGGGTTGGTTCCA  
 TCTTGCCGAGTCTGCCGAATGTGGATGGGAAGACCAAGAGGAGGAGCAAGGGCAGAGGGAAAGGGATCTTAA  
 AGAAGTCCTGGATGCCACACTCTTCTCTCTCTCCCTCTCAGAGGTCTCACTCGTGGTCTTCT  
 TTCCTGCCCTGCCTCCATCTCTCTGGGTGCTGGAAAGTGGAGGATTAGCTGAAGTTTGCTTCTCGGGCCTG  
 TCTGAATCTCATTGCTTCTGGGAGGACATAATTACCTGTCTAGCTTCTATCATCTTACATTCCCTGTAG  
 CCACTGGGACATATGTGGTCTCTAGCTCCTGTCTCCTCATGCCCTTGCTGGGTATGGCAGTGTAG  
 GGGGAAGGTATTGCTGTCAGAGGGCACTGACTTTCTAATGGTGTACCCAAAGGTGAATGTTGGAGACACAGTC  
 GCGATGCTGCCAAGTCCCGCGAGCCCTAACTATCCAGAGATCGCTGCGCTGCCAGGTCCCTGCATGGT  
 ATGAGCCCTCCC**ATG**TTCTGGGCACTTTGCTTCTCCCTCCAGGTGAATCTCAGCCCCCTCTCCACCCAAAGGTTC  
 ACATGGATCCTAACTACTGCCACCCCTCCACCTCCCTGCACCTGTGCTCCCTGGCTGGTCTTACCAAGGCTTC  
 TCCACCCCTCCCTATCTCAGGTATTCCCAGGTGGTGAAGGACCACGTGACCAAGCCTACCGCCATGCCAGG  
 GCCGAGTGGCTCACCTATTGAGTGAAGGGCTGGAGCAAGCCAGTGACTCACCTGCTGCCCTGGAATCAGCCT  
 TTTCCCTATTAGACCTCAGCAGGGCAACAAGAGGCTCGTTGAGCAGGAGTGGCTGAGCAGTTGCCA  
 TCGCGGAAGCCAAGCTCGAGCATGGTCTCGTGGATGGCAGGACTCCACTGATGACTCCTATGATGAGGACT  
 TTGCTGGGGATGGACACAGACATGGCTGGCAGCTGCCCTGGGCCGACCTCCAGGACCTGTTACCGGCC  
 ACCGGTTCTCCGGCTGTGCGCCAGGGCTCCGTGGAGCCTGAGAGCGACTGCTCACAGACCGTGTCCCCAGACA  
 CCCTGTGCTCTAGTGTGAGCAGCTGGAGGATGGTTGTTGGCTCCCCGGCCGCTGGCTCCAGTGCTGG  
 GCGATGAGCTGCTCTGCCAAACTGCCAGGGAAAGTGCCTTCCGAGCCTGGGCCACTGGAGGCCCC  
 AGGACTCACTACAACACTGCCCTCACAGAGTCTGCCCTCCCCGGGGAGGAGGAGGCCAGCCCCCTGCAAGG  
 ACTGCCAGCCACTCTGCCACCACTAACGGCAGCTGGAACGGCAGCGGCAAGCCTGACCTGCCCTTCTG  
 GGGTGGTGTCTTAGATGAGGATGAGGAGCAGAGGAACAG**TGA**CCCACATCATGCCCTGGCAGTGGCATGCA  
 TCCCCCGCTGCTGCCAGGGCAGAGCCTCTGTGCCCAAGTGTGGCTCAAGGCTCCAGCAGAGCTCCACAGCC  
 TAGAGGGCTCTGGGAGCGCTCGCTCTCCGTTGTTGATGAAAGTGTGTTGGAGAGGGAGGCAGGGCTG  
 GGCTGGGGCGCATGTCCTGCCCTACTCCCAGGGCTTGGCGGGGGTTGCCCGGGGCTCTGGGGCATGGCTACA  
 GCTGCGCAGACAGTGATGTTCATGTTAAATGCCACACACATTTCTCTCGGATAATGTGAACCACTA  
 AGGGGGTGTGACTGGGCTGTGAGGGTGGGGTGGAGGGGCCAGCAACCCCCCACCCTCCCCATGCCCTCTC  
 TCTCTCTGCTTCTCCTCACTTCCGAGTCATGTGCACTGCTGTTGATGAAATCACCCCCACCTGGAGGGCTGG  
 CTCTGCCCTCCGGAGCCTATGGGGTGGCCGCTCAAGGGCCCTGCCAGCTGGGCTCGTGTGCTTC  
 ATTACACTCTCCATCGTCTCAAATCTCTCTTCTAAAGACAGAAGGTTGGCTGTTGATGCTGCTGTTGCTC  
 GGATCTCTCTCTGGAGGCTTGGAAATGATGAAAGCATGTACCCCTCCACCTTCTGGGGCCCTAATGG  
 GGCCTGGGCCCTTCCAAACCCCTCTAGGATGTGCGGGCAGTGTGCTGGGCCCTCACAGCCAGCCGGCTGCC  
 ATTACCGCAGAGCTCTGAGCAGGGAGGTGGAGAAAGGATGGCTGTTGCAAGAGCTGGGACTCATGTT  
 CTTCTAGAGAGGGCCACAAGAGGGCACAGGGGTGGCCGGAGTTGTCAGCTGATGCCCTGAGAGGCAGGAAT  
 TGTGCCAGTGTGAGTGACAGTCATGAGGGAGTGCTCTTCTGGGGAGGAAAGAAGGTAGAGCCTTCTGCTGAAT  
 GAAAGGCCAAGGCTACAGTACAGGGCCCGCCAGCCAGGGTGTAAATGCCACGTCAGTGAGGGCCTGGCAG  
 ATCCTGCATTCCAAGGTCACTGGACTGTACGTTTATGGTTGGGAAGGGTGGTGGCTTAAAGATTAAGGGC  
 CTTGTAGGCTTGGCAGGTAAAGAGGCCAACAGTAAGAACAGAGGCCAACGGCACAAGCATTCTATATATAAGT  
 GGCTCATTAGGTGTTATTGTTCTATTAAAGAATTGTTATTAAATTAATAAAAATCTTGTAAATCTC  
 TAAAA

## **FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSFPSHPKVHMDPNYCHPSTSLHLC  
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPALESAFSSY  
SDLSEGEQEAFRAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPSPDTLCSSLCSLEDGLLGSPARLASQLLGDE  
LLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER  
QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

## FIGURE 23

GGTCCTGGCGCTGTTACACAAGCAAGATAACGCCAGCCCCACCTAATTTGTTCCCT  
 GGCACCCCTCCTGCTCAGTGCACATTGTCACACTTAACCCATCTGTTTCTTAATGCACGA  
 CAGATTCCCTTCAGACAGGACAACGTGATATTCAAGTCAGTTCTGATTGTAAATACCTCCTAAG  
 CCTGAAGCTCTGTTACTAGCCATTGTGAGCTCAGTTCTCATCTGCAAAATGGGCATAA  
 TACAATCTATTCTGCCACATCAAGGGATTGTTATTCCCTTAAAAAAACCAATACCAAAG  
 AAGCCTACAATGTTGGCCTAGCCAAAATTCTGTTGATTCAACGTTGTTTATTCACTTCT  
 ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACACAGAACATTGCAGAAGTT  
 TTAAAACAATGGAAAATAACCTATTCTTGAAAGTGAAGCAAACTAAACTCAGATAAA  
 GAAAATATAACCACCTCAAATCTCAAGGCAGTCATTCCCTCCTTGAATCTACCAACAA  
 CAGCCACGGAATAACAGATTCTCCAGTAACTCATCAGCAGAGCATTCTGGCAGTCTAA  
 AACCCACATCTACCATTCCACAAGCCCTCCCTGATCCATAGCTTGTAAAGTGCCT  
 TGGAATGCACCTATAGCAGATGAAGATCTTGCCATCTCAGCACATCCAATGCTACACC  
 TGCTCTGTCTCAGAAAACCTCACTGGTCTTGGTCAATGACACCGTGAAAACCTCTGATA  
 ACAGTTCCATTACAGTTAGCATCCTCTTCAGAACCAACTCTCCATCTGTGACCCCCTG  
 ATAGTGGAACCAAGTGGATGGCTTACACAAACAGTGAAGTAGCTTCACTGGTTACCCCTTA  
 TCAAGAAAAACAACTCTACAGCCTACCTTAAATTACCAATAATTCAAAACTCTTCAA  
 ATACGTAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTGGGCCATTAGGT  
 GCTATTCTGGGTGTCTCATTGCTTACTCTGTGGCTACTGTGTTGTGAAAAAGGAAAAC  
 GGATTCAATTCCCCTCGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA  
 ATGCACCGAACCTTATGATGTGAGTTGGATTCTAGCTACTACAATCCAACCTTGAAT  
 GATTAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC  
 TCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAGCGTTAACAGCAAGTGTCTAC  
 CATCCTAGCCTTGTGACAAATTCTACATTCAAAAGTTACACAAAATTACTGTCACGTGGAT  
 TTTGTCAAGGAGAACATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
 CCAAAGGTTTCTTCTTACAATTGGCATCCTGAGGCATTACTAAGTAGCCTTAATT  
 TGTATTAGTAGTATTCTTAGTAGAAAATATTGTGGAATCAGATAAAACTAAAGATT  
 TCACCATTACAGCCCTGCCTCATAACTAAATAAAATTATTCCACCAAAATTCTAAA  
 ACAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCATATTCAAGATTGCAT  
 TTTCTTAAATGAAAATTGAAAGGGTGTGTTAAAGAAAATTGACTTAAAGCTAAAAGAG  
 GACATAGCCCAGAGTTCTGTTATTGGAAATTGAGGCAATAGAAATGACAGACCTGTATT  
 TAGTACGTTATAATTCTAGATCAGCACACACATGATCAGCCACTGAGTTATGAAGCTGA  
 CAATGACTGCATTCAACGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT  
 TCTTAAAGTCTCAAAGGTTGGAAATTAACTTGTCTTAATATATCTTAGGCTTCAA  
 TTATTGGGTGCCTTAAAACCTCAATGAGAATCATGGT

## **FIGURE 24**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLLTIVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNSA
MPESEENARDGIPMDDIPPLRTSV
```

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 235-262

**N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311

## FIGURE 25

AACAGGATCTCCTTTGCAGTCTGCAGGCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
 AGCCCGAAGATTCACTATGGTGAAAATCGCCTTCATAACCCCTACCGCCGTGAAAAGGAGG  
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC  
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
 CTTAGGCCTTCATTCATCTTGGCAGGACTTATTGTTGGAGCCTGCATTACAAGTACT  
 TCATGCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTGATTCTGAGGATCCTGCA  
 AATTCCCTCGTGGAGGAGAGCCTAACCTCCTGCCTGTGACTGAGGAGGCTGACATTGCA  
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTCTGTGATAGTGACCTGCA  
 CAATTATTGACTTTGAAAAGGAATGACTGCTTACCTGGACTTGTGCTGGAACTG  
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTTTGG  
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTCAGAAGACCTAGTTGCTG  
 TGGAGGAAATTGATGTTAGTAACCTTGGCATCTTACCAACTTGCAATAACAGA  
 AAGTCCTCCGCCTCGTCGCAGAGACCTCTGCTGGTTCAACAAACGTGCCATTGATAA  
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTATTGTTGAGACCAAGATCTGTCAAGAGT  
AAGAGGCAACAGATAGAGTGTCTGGTAATAAGAAGTCAGAGATTACAATATGACTTAA  
 CATTAAGGTTATGGGATACTCAAGATATTAACATGCATTACTCTATTGCTTATGCTTT  
 AAAAAAAGGAAAAAAACTACTAACCAACTGCAAGCTTGTCAAATTAGTTAAT  
 TGGCATTGCTTGTGAAACTGAAATTACATGAGTTCTTTCTTGATTTAG  
 GTTTAGATTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCC  
 GTTGTGTTGTTGTTGTTGTTCTTTCTTTAAGTAAGCTTCTTATTGATCTTATG  
 GTGGAGCAATTAAAATTGAAATATTAAATTGTTGAACTTTGTGAAATTATA  
 TCAGATCTAACATTGTTGGTTCTTTGTTCTTCAACTTGTACAACCTTCTGAAATTAGA  
 AATTACATCTTGCAGTCTGTTAGGTGCTCTGAATTAACTGACTTATATGTGAAACAAATT  
 TTCATGAGACAGTCATTAACTAATGCAGTGAATTCTTCACTACTATCTGTATTGTGG  
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTAGGTTATGAATTCTACAA  
 CCCTATAATAAATTACTCTACAAAAA

## **FIGURE 26**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVALLSRTVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDPAAIIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFYQLCNNRKSFRLRRRDLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

## **FIGURE 27**

## **FIGURE 28**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEKGSQEGDQEVTQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV
```

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248

## **FIGURE 29**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA  
 GGGAGGACAGGGAGTCGGAAAGGAGGAGCACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG  
 GCAAGGAGGAGACCCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGCTGGCAGAG**ATG**  
 AAGTTCCAGGGGCCCTGGCCTGCCTCTGCTGGCCCTCTGCCTGGCAGTGGGAGGGCTGG  
 CCCCTGCAGAGCGGAGAGGAAAGCACTGGACAAATATTGGGAGGCCCTGGACATGGCC  
 TGGGAGACGCCCTGAGCGAAGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGCT  
 GGCTCTAAAGTCAGTGAGGCCCTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG  
 GCAGGTTCCAGGCTTGGCGCAGCAGATGCTTGGCAACAGGGCAGGGAAAGCAGGCCATG  
 CTCTGGAAACACTGGGACGAGATTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCA  
 GATGCTGTCCCGGCTCCTGGCAGGGGTGCCTGCCACAGTGGTCTTGGAAACTTCTGG  
 AGGCCATGGCATCTTGGCTCTCAAGGTGGCCTGGAGGCCAGGGCAATCCTGGAG  
 GTCTGGGACTCCGTGGTCCACGGATACCCGGAAACTCAGCAGGCAGCTTGGAAATGAAT  
 CCTCAGGGAGCTCCCTGGGTCAAGGAGGCAATGGAGGCCACCAAACCTTGGACCAACAC  
 TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTCAGTGAGAGGCCAGCAACCAGAATGAAGGGT  
 GCACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGAGGCAGCGGC  
 TCACAGTCGGCAGCAGTGGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG  
 TGGCAGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGA  
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGA  
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGA  
 TCCAGCACCGGCTCCTCCGGCAACCACGGTGGAGCGGGAGGAAATGGACATAAAC  
 CGGGTGTAAAAGCCAGGGAAATGAAGCCCGGGAGCGGGAAATCTGGATTCA  
 GAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATGCCCTGG  
 GGCTCTGGAGACAATTATCGGGGCAAGGGTCAGCTGGGAGCTGGAGGAGGTGACGCTGT  
 TGGTGGAGTCATACTGTGAACCTGAGACGTCTCCTGGATGTTAACTTGA  
 GACACTTCT  
 GGAAGAATTAAATCCAAGCTGGTTCATCAACTGGATGCCATAAACAAAGGACCAAGAGA  
 AGCTCTCGCATCCCG**TGA**CCCTCCAGACAAGGAGCCACCAGATTGGATGGAGCCCCACACT  
 CCCTCCTAAACACCACCCCTCATCACTAATCTCAGCCCTGCCCTGAAATAACCTTA  
 GCTGCCCAACAA  
 AAA

## FIGURE 30

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSGSSGGSSGGSSGGSSGSGSNGSRGDGSESSW
GSSTGSSSGNHGGSGGGNGHPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLI
GGSGDNYRGQGSSWGSGGDAVGGVNTVNSTSPGMNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP

```

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389, 387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

## FIGURE 31

GACCGGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGCGGTGCTCACCG  
 TGCCTGGCTGGAGTTCTCTCCTTGCTGACCATGTTGTCCTGCTGAAATATTACCGGGACATCTTCA  
 CTCTCCTGCTGCCCTGACCGAGCTGGTGTGCGAGAGAGTGAGGGAAAGAT**TG**TGTTCTGAAACAAGC  
 TGCTGCTACTTGCTGCTGGCTGGCTTCCAGATTCCCAGTGAGGACTTGTTCTTCTGGAAGAGG  
 GTCCCTCATATGCCCTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGACAAATGCGCTGTGGTGGACCGAC  
 AGCTGCTCTACACCTGCTGCCCTACATGGAGAGCTGGAAACTGCTCGCTCGTGGTGTCAAGGAGTAGTG  
 GACGGAGTGGGGCTTCATGAGGAAATCACCCCCACCACCTACCAACAGGCCCTGGGAGGCCAGCCTTCCCAGACCA  
 GCCAGGGCTGCAGGCACAGCTGCCAGGCCCTTCCACAACCAGGCCCTCCTGCGCCGGACCGTAGAGT  
 TCGTGGCAGAAAGAATTGGATCAAACATATCAAGGCTACACTGTTGGCAGATCTGGTGCAGCAG  
 CAGAGTCACCTCTCCAAGAGCAGCTGGTACACAGGGAGAGGAAGGGGGAGACCCAGGCCAGCTGGAGATCT  
 TGTGTTCCCAGCTGTGCCCTCACGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAGGAAGAGGCCCTG  
 GGGCTGTGCGGGCGTCTCCAGAGGGAGACCCGGCAGGCCCTGAGCAGTGCAAGAGAACATTGCTGTGGGGC  
 TTGCAACAGAGAAAGCCTGTGCTGGCTGTCAGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG  
 TGAGTCGCACACTTCGAGCCCAGGTCTGAAACCTGCTGCCGGGGAGCGGAGGGCTGCTCCCGGCC**TGAC**  
 GTGCTCTCTGGCCGTGGGCCAGGGACCTGACGAGGGAGTCTCCCAGAGCATCTGGAACAGCTCTAGGC  
 CAGCTGGCCAGCAGCTGCCGTGCCAGTTCTGTGAGCAGCATCTGCCAAAGTGCTCTGTG  
 GAGTTAGCTCCCTCTCGTGCAGATCAAATTCTATCTTAGGGCCCCGGCACAGTACAGGCTGGAGAGAGGG  
 CAGGCTCGAAGGCTCTGCACATGCTGCTTCCTGTGAAAGGAAGACTTCAGGGCCGGTCCGCTGCAGCTG  
 CTGCTGAGCCCAAGAAATGTGGGCTTCTGGCAGACACAAGGCAAGGGAGTGGACTTGCTGCTATTCTGCTA  
 CGGGAGCTGGTGGAGAAGGGTCTGATGGGACGGATGGAGATAGAGGCTGCCCTGGCAGCCCTCACAGGCCAG  
 TGGCCAGGGACTTGCTGAAGAATTAGCAACACTGCTAATCTGTTCTAGCCGAGCCCACCTGCCAGAACCC  
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTCGCCAGAGCTAGGGCTGAGAACAGTGGCC  
 CTGCTCTGGGATTGACCCAGAACCCCTGGACCCCCGCTCACGAGGAGGCCAAGTGCCTAACAGACCCCTCAC  
 TGGTTGGGTGAGCTGGTCTACAGTCAGACTTCTGCTTAAGGGTGTCACTGCCCTGGCATCCCCAACAGCGA  
 ATCCTAGAGGAAGGGAGAGTGGCTGATTGGGATTATGGCAGAAAAGTCCAGAGATGCCAGTCTGGAGTAGAA  
 GAGGTGGTGTGTTATCTCTGGATAACTAAATGAAATGAGGTGTGTTGCTGTCACAGAGGCAATCAAGCCT  
 CATTGCTATCCCAGCATCTTAAACACTTGTAGTCTGGAAATCATGACAGAGGCAATGACTCCTGCTTAAC  
 TTATGAAGAAAGTAAACATGAATCTGGAGTCTACATTCTTATCACCAGGAGCTGGACTGCCATCTCCTT  
 ATAAATGCCTAACACAGGCCGGTCTGGTGGCTCATGCCGTAAATCCCAGCACTTGTGAGAGGCTGAGGTGGCG  
 GACTGCCTGAGGTCAAGGAAATTCAAGACCAGGCCGGCAACATGGAAAACCCATCTCTACTAAAATAAAAAA  
 TTATTAGCTGGGATGGTGGTGTGCTGTAATCCCAGCTACTCAGGAGGATGAGGAGACCTGTTGAAC  
 CTGGAGGTGGAGGTTGCACTGAGGCCAGGTGCCACACTGCACTCCAGTCTGGTAACAGAGCGAGACTTTCTAG  
 AAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTCCCCCTGTACCTTCAGCCCTG  
 TGCAGGTAGTAACCTCTGAGACCTCCCTGACCGAGGCCAACAGGGCATTTAGAGCTTTTAAATAAA  
 CTGGTTTCTTAAAAAAGGGCGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  
 TTTTTTTTTTTTAAAGGGCTTTATTAAAATCTCCCACAGATGGCTCTGCAATCTGCCACAGCTC  
 TGGGGCGTGTCTGAGGAAAGGCCCTGTTTCCCTGAGGCGGGCTGGCTTGTCCATGGGTCCGGAGCTG  
 GCCGTGCTGGGCCCTGGCTGTGCTAGCTGCTTCTGCCGGCACAGAGCTGCCGGCTGGGGGCCACCGGG  
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCTGCTCTTAACCGACACCCCTGAGGTGCTCTGAGATGCTG  
 GGTCCACCCCTGAGTGGCACGGGGAGCAGCTGTCGGCGGTGCTCTCYAGGCCAGTCTGGGAAACTAAGCTC  
 GGGCCCTTCTTGCAAAAGAGCAGGATGGGTGGTGTGGGGACTCATGGGAAATGCCGTGAGGAGCTACGTGT  
 GAAGAGGGCGCCGTTGGCTGAGCGGCCCTGGAGGCCCTCTCCTGAGGCCAGTCTCCCTTCCGTCTA  
 ATGAAGAACATGCCGTCTGGTGTCTCAGGGCTATTAGGACTTGCCCTCAGGAATGGCCCATGCCCCCTGCTGCCGTG  
 GTTATTTCACAACCTGTCCTGCGACGTTGGCTGGCACGTCTGAAGAATGGCCCATGCCCCCTGCTGCCGTG  
 GTCGCGGTGGAGTGCAGCCAGGGCGCACAGCTGCCCTGGGGTGGAGGGAGGCCACCCGGAGGG  
 CCTCACAGGAAGTTGGCTCCCGCACCAAGGCAGGGGGCTCCCGCCGCCGCCACCACCGTCCAGG  
 GGCCGGTAGACAAAGTGGAAAGTCGCGCTTGGGCTGCGCAGCAGGTAGCCCTGATGCAAGTGCAGGAGC  
 TCGTCCGCCAGCTGGAAGCAGCGCCGTCCACAGCACGAACAGCCGGTGCCTC

## FIGURE 32

MCFLNKLLLLAVLGWLQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC  
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP  
SLRRTVEFVAERIGSNCVKHIKATLADLVRQAESLLQEQLVTQGEEGGDPAQLLEILCSQL  
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL  
IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282

## **FIGURE 33**

TCCCTTGACAGGGTCTGGTGGCTGGTCAGGGCTACTGAAGGCTGTCTGATCAGGAAACT  
AAGACTCTCTGCTTGGCACAGCAGTCTGCAGCTCCTGAGGTGTGAACCCACATCCC  
TGCCCCCAGGGCACCTGCAGGACGCCACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**  
AGTAGCAACAAAGAGCAGCGGTAGCAGTGTGATCCCTTTGCCCTCATCACCACCT  
CATCCTCTACAGCTAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCCGGCGTA  
GCCGCCACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC  
AACAAAGACACTGCCCTCGGTGCCACCAAGTGTGATTGTAGCAGCAGCTCCAGCCACCTGCT  
GGGCACCAAGCTGGCCCTGAGATCGAGCGGGCTGAGTGACAATCCGATGAATGATGCAC  
CCACCACTGGCTACTCAGCTGATGTGGCAACAAGACCACCTACCAGCTCGTGGCCCATTCC  
AGTGTGTTCCCGGTGCTGAGGAGGCCCAAGGAGTTGTCAACCGGACCCCTGAAACCGTGT  
CATCTCTGGGGGCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCCTGTGATCC  
AGCGAGCGGGCCTGGTGTCCCCAACATGGAAGCATATGCCGTCTCTCCGGCCGATGCGG  
CAATTGACGACCTCTCCGGGTGAGACGGCAAGGACAGGGAGAAGTCTCATTGTTG  
GAGCACAGGCTGGTTACCATGGTATCGCGGTGGAGTTGTGACCACTGCATGCTATG  
GCATGGTCCCCCAACTACTGCAGCCAGCGGCCGCCCTCAGCGCATGCCCTACCAACTAC  
TACGAGCCAAGGGGCCGACGAATGTGTCACCTACATCCAGAATGAGCACAGTCGAAGGG  
CAACCACCACCGCTTCATCACCAGAAAAGGGTCTCTCATCGTGGGCCAGCTGTATGGCA  
TCACCTCTCCACCCCTGGACC**TAG**GCCACCCAGCCTGTGGACCTCAGGAGGGTCAG  
AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTCTGGCCAATCAAGGCTTG  
CTGGAGTGTCTCCAGCCAATCAGGGCCTGAGGGAGATGTATCCTCCAGCCAATCAGGGCC  
TGGGAATCTGTTGGGAATCAGGGATTGGAGTCTATGTGGTTAATCAGGGGTGTCTTC  
TTGTGAGTCAGGGCTGCGCACAGTCATCAGGGTAGAGGGGTATTTCTGAGTCATCTG  
AGGCTAAGGACATGTCCTTCCATGAGGCCTGGTCAGAGCCCCAGGAATGGACCCCCCA  
ATCACTCCCCACTCTGCTGGATAATGGGGCTGTCCCAAGGAGCTGGAACTTGGTGT  
CCCCCTCAATTCCAGCACCAGAAAAGAGAGATTGTGTGGGGTAGAAGCTGTCTGGAGGCC  
GGCCAGAGAATTGTGGGGTTGTGGAGGTTGTGGGGCGGTGGGGAGGTCCAGAGGTGGGA  
GGCTGGCATCCAGGTCTGGCTCTGCCCTGAGACCTTGGACAACCCCTCCCCCTCTGG  
CACCTCTGCCACACCACTGGTCTGCTCCCCGTCTGGACCCCTCCAGCCACTATCCCTG  
GTGCCCTGGTCTGCTCTCCCCGTCTGGACCCCTCCAGCCACTATCCCTGCTGGAAAGGCT  
CAGCTCTTGGGGGTCTGGGTGACCTCCCACCTCCTGGAAAACCTTAGGGTATTTTG  
GCAAACCTCTCAGGGTGGGGACTCTGAAGGAAACGGGACAAACCTTAAGCTGTTTCT  
TAGCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCCTCTTCTGCCCT  
CTAGCAGGGAGGTTTCCAACCTGTTGGAGGCGCTTGGGGCTGCCCTTGTCTGGAGTC  
CTGGGGCTCCGAGGGCTCCCTGACCCCTGTCGCTCTGGATGGCTGTCGGAGCTGT  
ATCACCTGGTTCTGCTCCCTGGCTCTGATCAGGCACTTATTAAAGCTGGGCCAGTGG  
GGTGTGTTGTCCTGCTCTGGAGCCTGGAAGGAAAGGGCTCAGGAGGAGGCTGTGA  
GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTATGGGTGG  
GGCGGGTGAUTGCCCAACTGGTTTGTAAATGATTGTACAGGAATAAACACACCTACGC  
TCCGGAAA

## **FIGURE 34**

MSSNKEQRSAVFVILFALITILYLSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
GNKTLPSRCHQCVIVSSSSHLLGPKGPEIERAECTIRMNDAPTGYSADVGNKTYRVVAH  
SSVFRVLRRPQEFDVNRTPETVFIFWGPPSKMQKPGSLVRVIQRAGLVFPNMEAYAVSPGRM  
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPRLQRMPYH  
YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

## **FIGURE 35**

## FIGURE 36

MLRGMTAWRGMRPEVTIACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVLGCVVEPP  
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL  
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQ  
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRSTAEEAARIIYPPEAQTIIVTKGQSL  
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA  
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQLRLS  
 RRALRVLSMGPEDEGVYQCMAENEVGSAAHVQLRTSRPSITPRLWQDAELATGTPPVSPSK  
 LGNPEQMLRGQPALPRPPTSVGAPSPKCPGEKGQGAPAEAPIIILSSPRTSKTDSYELVWRPR  
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE  
 GQTAMVTFRGRRPKPEIMASKEQQIQRDDPGASPQSSQPDHGRLSPPPEAPDRPTISTASE  
 TSVYVTWI PRGNGGFPIQSFRVEYKKLKKVGDWILATS AIPPSRLSVEITGLEKGTSYKFRV  
 RALNMLGESEPSAPS RPYVVSGYSGRVYERPVAGPYITFTDAVNETTIMLKWMYIPASNNNT  
 PIHGFYIYYRPTDSDNDSDYKKDMVEGDKYWHSISHLQPETSYDIKMQCFNEGGESEFSNVM  
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL  
 IIVTFIPFCLWRAWSKQKHTTDLGFPRTSALPPSCPYT MVLGGLPGHQASGQPYLSGISGRA  
 CANGIHMNRGCP SAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK  
 SSPDEGSFLYTL RDDSTHQLLQPHDCCQRQECPAAVGQSGVRRAPDSPVLEAVWDPPFHSG  
 PPCCCLGLVPVEEV DSDSCQVSGGDWCPQHPVGAYVGQEPMQLSPGPLVRVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879

## FIGURE 37

CGGGAGGCTGGGTCGTATGATCCGGACCCATTGTCGGCCTCTGCCCATGCCCTGCTCCTC  
 CCAGGCTCCCGCGGCCGACCCCCCGCGAACATGCAGCCCACGGGCCCGAGGGTTCCCGCGC  
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCGGCAGC  
 CCGTAACCCGCGCGGAGACCACGCCGGCGCCCCAGAGCCCTCTCACGCTGGCTCCCC  
 AGCCTCTTACACGCCGGGTGCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG  
 CACCCCCAAAACCTGGACCTCGGGTCGCGCGAGGCCCTGATGCGGAGTTCCACTCG  
 TGGACGGCCACAATGACCTGCCAGGTCCTGAGACAGCGTTACAAGAAATGTGCTTCAGGAT  
 GTTAACCTGCGAAATTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT  
 GGGTGCCAGTTCTGGTCAGCCTCCGCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC  
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTCCTACTCTGAACACTCGAGCTT  
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATGGCGTGNAGGG  
 TGGTCACTCACTGGACAGCAGCCTCTGTGCTGCGCAGTTCTATGTGCTGGGGTGCCT  
 ACCTGACACTTACCTCACCTGCAGTACACCATGGCAGAGAGTCCACCAAGTTCAGACAC  
 CACATGTACACCAACGTCAAGCGGATTGACAAGCTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
 CCGCCTGGCATGATGATAGATTGTCCTATGCATGGACACCTGATAAGAAGGGCCTGG  
 AAGTGTCTAGGCTCTGTGATCTTCTCCACTCAGCTGCCAGAGCTGTGTCAGACT  
 TTGAATGTTCCCGATGATATCCTGCAGCTCTGAAGAACGGTGGCATCGTGTGACACT  
 GTCCATGGGGTGCTGCAGTGCAACCTGCTGCTAACGTGTCCTGTGGCAGATCACTTG  
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATGGGATTGGTGAAATTATGACGGACT  
 GGCGGTTCCCTCAGGGGCTGGAGGATGTGTCACATACCCAGTCCTGATAGAGGAGTTGCT  
 GAGTCGTASCTGGAGCGAGGAAGAGCTCAAGGTGTCCTCGTGGAAACCTGCTGCGGGTCT  
 TCAGACAAGTGGAAAAGGTGAGAGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTT  
 CCATATGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGGC  
 TACTCATCTGGAGGTGACCAAGCAGCCAACCATGGTCCCCTGGAGGTCTCAAATGCCT  
 CCCATACCTTGTCCAGGCCTTGTGGCTGCCACCATCCAACCTCACCCAGTGGCTC  
 TGCTTGACACAGTCGGTCCCCAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCCT  
 AGTTCAATTACAAGCATATGCTGAGAATAACATGTTACACATGGAAAA

**FIGURE 38**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRLLLLLRLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTPGLTPGTPKTLDLRGRAQALMRSFPLVDGHNDLHQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLAQCLIGVXGGHSLDSSLVLSFYVLGVRYLTFTCSTPWAESSTKFRHHMYTNVSLT
SFGEKVVEELNRLGMMIDLDSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYGQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRPWRSSNASPYLVPGLVAAATIPTFTQWLC

```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

## FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
 TCCCTCTATGACTGCAATGTGAGGTGTCGGCTTGCTGGCCCAGCAAGCCTGATAAGC**ATG**  
 AAGCTCTTATCTTGGTGGCTGTGGTGGGTGTTGCTGGTCCCCAGCTGAAGCCAACAA  
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGCACA  
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCAGGCCA  
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
 CACCACCACCATCAAGGTACATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT  
 ACATGGCCTTCCTGATGCTGGTGGACCCCTGTGATCCGAAAGCCGGATGCATACACTGAGCAA  
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTATGGCAGCAGCTGCTGCATCCCTCGG  
 GGGACCCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC  
 AGGTGCAGGAGCAGCGGAAGACAGTCTCGATGGCACAAAGATGCTCAGC**TAG**ATGGGCTGG  
 TGTGGTTGGGTCAAGGCCAACACCATGGCTGCCAGCTCCAGGCTGGACAAAGCAGGGGG  
 CTACTTCTCCCTCCCTCGGTTCCAGTCTTCCCTTAAAGCCTGTGGCATTTCCTCCTT  
 CTCCCTAACCTTAGAAATGTTGACTTGGCTATTGATTAGGAAAGAGGGATGTGGTCTCT  
 GATCTCTGTTGTCTTCTGGTCTTGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA  
 ATGGAGACATTGAGGCCGCTCAGGAGTGGATGCGATCTGTCTCCTGGCTCCACTCTG  
 CCGCCTCCAGCTCTGAGTCTGGGAATGTTACCCCTGGAAAGATAAAGCTGGGTCTTCA  
 GGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTGACATGTGTTCTTCTGCAGTG  
 GTTCTTATCACCAACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCAGTGGCTTCAGGGTGCAGTGGA  
 AGCTGGTGGTGTGACTTCCCTGTGCACTTCTCGCACTGGGCATGGAGTGCCATGCATACT  
 CTGCTGCCGGTCCCTCACCTGCACTTGAGGGTCTGGCAGTCCCTCTCCCCAGTGTGTC  
 CACAGTCAGTGGCCAGACGGTCGGTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA  
 CACCAAGCCCCCTGTACTTGGGTTGCCTCTTGTCCCTGAACCTCGTTGACCGATGGAA  
 GAGAAAATTTGTCCTTGTCTTAGAGTTGTGTAAATCAAGGAAGCCATCATTAAATTG  
 TTTTATTCCTCTCA

## **FIGURE 40**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGHDVEAYCLLCECRYEERSTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

**Important features:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50

## FIGURE 41

AGCGGGTCTCGCTGGGTCCGCTAATTCTGCCTGAGGCCTGAGACTGAGTCATAGGTCTGGGTCCCCGA  
 ACCAGGAAGGGTGAGGGACACAATCTGCAAGCCCCCGCACCAAGTGAGGGCCCGTGTGGGTCTCCCC  
 TCCCTTGCATTCCCACCCCTCGGCTTGCCTCTCCCTGGGGACCCCTCGCCGGAGATGGCCGCTGATG  
 CGGAGCAAGGATTGCTCTGCTCCTACTGGCCGGTGTGATGGTGGAGAGCTCACAGATCGGCAGT  
 TCGGGGCAAACCTCAACTCCATCAAGTCTCTGGGGGGAGACGCCTGGTCAGGCCAATGATCTGCG  
 GGCATGTACCAAGGACTGGCATTGGCGAGTAAGAAGGGCAAAACCTGGGCAGGCCAACCTGTAGCAGT  
 GATAAGGAGTGTGAAGTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATGGCCTGCATGGTGTGCGGAGA  
 AAAAAGAAGCCTGCCACCGAGATGGCATGTGCTGCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT  
 ACTGAAAGCATCTAACCCCTCACATCCCAGCTGGATGGTACTCGGCACAGAGATGAAACCACGGTCATTAC  
 TCAAACCATGACTGGGATGGCAGAATCTAGGAAGACACACACTAAGATGTACATATAAAGGCATGAAGGA  
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTGCTGTGCTGTCATTCTGGACCAAAATCTGCAA  
 CCAGTGCTCCATCAGGGGAAAGTGTACCAAACAACGCAAGAAGGGTCTCATGGCTGAAATTTCAGCGT  
 TGCAGACTGTGCGAAGGGCCTGCTTGCAGAAGTATGGAAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG  
 TGTCAGAAAATTTGATACCAATTGAGGAACATCATCAATTGAGACTGTGAAGTTGTATTTAATGCATTATAG  
 CATGGTGAAAATAAGGTTCAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAA  
 AAAGGGAGAAAAGAACATGAACTGAATAGATTAGAATGGGTGACAATGCACTGCAGTCAGCCAGTGTTCATTATG  
 CAACTTGTCTATGTAATAATGTACACATTGTGAAAATGCTATTATAAGAGAACAGCACAGTGGAAATT  
 ACTGATGAGTAGCATGTGACTTTCAAGAGCTTAGGTTGTGCTGGAGGAGGGTTCCCTCAGATTGCTGATTGC  
 TTATACAAATAACCTACATGCCAGATTCTATTCAACGTTAGAGTTAACAAAATACTCCTAGAATAACTTGT  
 TACAATAGGTTCTAAAATAATTGCTAAACAAGAAATGAAACATGGAGCATGTTAATTACACAGAAAAT  
 TACCTTTGATTGTAACACTACTTCTGCTGTCATCAAGAGCTTGGTAGATAAGAAAAAAATCAGTCATAT  
 TTCCAAATAATTGCAAAATAATGGCCAGTTGTTAGGAAGGCCTTTAGGAAGACAAATAACAAACAAACAG  
 CCACAAATACTTTTCAAAATTAGTTTACCTGTAATTAAAGAATGATACAAGACAAAACAGTTCC  
 TTCAGATTCTACGGAATGACAGTATCTCTTTATCTGATTCTGCTGTCATGCAATTATTTCCA  
 AACTATACCCATAAATTGTGACTAGAAAATACTTACACAGAGCAGAATTTCACAGATGCCAAAAAATTAAA  
 GATGTCAATATATGTGAAAAGAGCTAACAGAGAGATCATTATTCTTAAAGATTGGCCATAACCTATATT  
 GATAGAATTAGATTGGTAAATACATGTATTGATACATACACTCTGTGTTAATAGAGACTTAAGCTGGATCTGACTG  
 CACTGGAGTAAGCAAGAAAATTGGAAAACCTTTGTTGTCAGGTTTGGCAACACATAGATCATATGTCTG  
 AGGCACAAGTGGCTGTCATCTTGAAACCAGGGGATGCACAGTCTAAATGAATATGCACTGGATTTGCTAT  
 CATAATATTACTATGCAGATGAATTGAGCTAACAGAGAGATCATTCTGCTGTTGTCAGGTTTGGCAACACATAG  
 TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTCAAAATGTAACCTGCTGAAAGTAGACAGAGTAG  
 TTTATTGCCCTCTATAAGCTCTGACTAGCAATGGCATCATTCCAAATTCTCCAAACCTCTGCAGCATCTG  
 CTTTATTGCCAAAGGGCTAGTTGTTCTGCAGCCATTGGTAAAAAATATAAGTAGGATAACTTGAA  
 ACCTGCATATTGCTAATCTATAGACACCACAGTTCTAAATTCTTGAACCAACTTTACTACTTTTTAAACTT  
 AACTCAGTTCTAAATACTTTGTCGGAGCACAAAACAATAAAAGGTTATCTTATAGCTGACTTTAAACTTTG  
 TAGACCACAATTCACTTTTAGTTCTTTACTTAAATCCCCTGCACTGCTCAAATTAAAGTTCTCCAGTAG  
 AGAGTGAAGTTGAGCTGTATATCTATTAAAATTTCACACTCCACATATTACTAAGATGATTAAGACTTA  
 CATTCTGCACAGGTCTGCAAAACAAAATTATAAAACTAGTCCATCCAAGAACCAAGTTGTATAAACAGGT  
 TGCTATAAGCTGTGAAATGAAATGGAACATTCAATCAAACATTCTTATATAACAATTATTATTTACAAT  
 TTGGTTCTGCAATATTCTTATGTCACCCCTTTAAAATTATTGAAAGTAATTATTTACAGGAAATG  
 TTAATGAGATGTTCTTATAGAGATATTCTTACAGAAAGCTTGTAGCAGAATATTTGCAGCTATTGAC  
 TTTGTAATTAGAAAAATGATAAAGATAAAATCTATTCTCCTCTAAACACTGAAAAA  
 AAAA

## **FIGURE 42**

MAALMRSKDSSCCLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQGSSACMVCRKKRCHRDGMCCPSTRCNN  
GICIPVTESTITPHIPALDGTRHRDRNIGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS  
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS  
SKARLHVCQKI

**Signal peptide:**

amino acids 1-25

100 200 300 400 500 600 700 800 900 1000

## FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAAATCCACCTACCTGGCCTCCAAA  
 GTGTTGGGATTACAGGCCTGAGCCACCGCGCCGGCAACATCACGTTTAAAAATTGATT  
 TCTTCAAATTATGGCAAATATTCCTCCCTTAACCTCTTATGTCAGAAATGAGGAAGGA  
 TAGCTGCATTTAGTCAGTTTCATTGCATAGTAATATTCATGTAGTATTCTAAG  
 TTATATTTAGTAATTATGTTAGATTATAGGTTAACATACTTGTGAAAATACTTG  
**ATGT**GTAAAGCCTGGCAGAAATTCTGTATTGTTGAGGATTGTTCTTTATCCCCCT  
 TTTAAAGTCATCCGCTTGGCTCAGGATTGGAGAGCTGCACCAACAAATGGCAAACA  
 TCACCAAGCTCCCAGATTTGGACCAGTTGAAAGCTCCGAGTTGGCCAGTTACCACC  
 CCAAGTACACAGCAGAATAGTACAAGTCACCCCTACAACACTACTACTTCTGGGACCTCAAGCC  
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTGACTCAAATCTCAACCTGAGCCATCCC  
 CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTCACTGTTCTCCT  
 CCTGGTTGGAGTCCTTCCTCCAGGCAAACCTCGAGAATCAACACCTGGAGACAGTCC  
 CTCCACTGTGAACAAGCTTGCAGCTCCAGCACGACCATTGAAAATATCTGTGTCTG  
 TCCACCAGCCACAGCCAAACACATCAAACCTGCTAACGGCGGATACCCCCAGCTCTAAAG  
 ATCCCCAGCTCTGCAGTGGAAATGCCTGGTCAGCAGATGTCACAGGATTAAATGTGCAGTT  
 TGGGGCTCTGGAATTGGGTAGAACCTCTCTGAATTGGATCAGCTCCAAGCAGTG  
 AAAATAGTAATCAGATTCCATCAGCTGTATTGAAGTCTTAAGTGAGCCTTGAAATACA  
 TCTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTATTACCTCTG  
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTCCTTATGACC  
 AGAGTTCTGTGCATAACAGGATCCCACACAAAGCCCTGTGAGTCATCAGAGTCAGCTCCA  
 GGAACCATCATGAATGGACATGGTGGTCAGTCAGCAGACACTAGACAGTAAGTATAG  
 CAGCAAGCTACTCTGTATGGCTGGTGCACCAACAAACAGAGGAAGAGGATAGTCACGTGA  
 TGTGGAAAACACCAGTTGGTCAATGGCTCATTCTG**TAAA**AGCAGCCCTTGTCTTTGT  
 TTTGGACCAGGTGTGGCTGTGGTATTAGAAATGTCTTAACCACAGCAAGAAGGGAGGT  
 GGTGGTCTCATATTCTCTGCCCTAACAGACTGCACCAAGTGCAGCATACTGATGCAT  
 TTTAAAGATGCTGGGCCAGGCAGGGTGGCTGATGCCATAATCCAGTGCTTGGGGGCC  
 AAGGCAGGCAGATTGCCAACAGCTCAGGAGTTGAGACCACCCCTGGCAACATGGTAAACTC  
 TGTCTCTACTAAAATACGAAAAACTAGCCGGGTGGTGGCGCGCGTGCCTGTAATCCCAG  
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGCTACAAAGTGAGACTCC  
 GTCTGAAAAGA

## **FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTP  
PSTQQNSTSHPTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP  
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASK  
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
SLSMTSAVQNSTYTTSVITSCSLTSSSILNSASPVAMSSSYDQSSVHNRIPYQSPVSSSESAP  
GTIMNGHGGGRSQTLDSKYSSKLLSWLVPKTQRKRIAHVMWKT P V G Q W L I R

### Signal peptide:

amino acids 1-24

卷之三

## **FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGCTGGCGGGGCC **ATG** GCGCTGCCATCCGAATCCTGCT  
 TTGGAAACTGTGCTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG  
 ACGCGGGCTGTACACCTGCAACCTGCACCACACTACTGCCACCTCTACGAGAGCCTGGCC  
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCGCTACTGGGACGGCGAGAAGGA  
 GGTGCTGGCGGTGGCGCGCGCACC CGCGCTTCTGACCTCGGTGAACCGCGGGCACGTGT  
 GGACCGACCGGCACGTGGAGGAGGCTAACAGGTGGTGCACTGGGACCGGCAGCCGCCGGG  
 GTCCCGCACGACCGCGCGACCGCCTGCTGGACCTCTACCGTCGGCGAGCGCCGCCCTA  
 CGGGCCCTTTCTGCGCACCGCGTGGCTGTGGCGCGGATGCCTTGAGCGCGGTGACT  
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCCGACGAGGGCACCTACTCCTGCCACCTGCAC  
 CACCATTACTGTGGCCTGCACGAACGCCGCTTCCACCTGACGGTCGCCAACCCACGC  
 GGAGCCGCCCCCGGGCTCTCCGGCAACGGCTCCAGCCACAGCGGCCAGGCCCCAGGCCAG  
 ACCCCACACTGGCGCGGCCACAACGTATCAATGTATCGTCCCCGAGAGCCGAGCCCAC  
 TTCTCCAGCAGCTGGCTACGTGCTGCCACGCTGCTGCTTCTCATCCTGCTACTGGTCAC  
 TGTCCCTGGCCGCCCGCAGGCGCCGGAGGCTACGAATACTCGGACCAGAAGTCGGAA  
 AGTCAAAGGGGAAGGATGTTAAC TTGGCGAGTTGCTGTGGCTGCAGGGGACCAGATGCTT  
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAAACATCCTGAAGGAGAGGGCGGAGCT  
 GGCCACAGCCCCCTGCCCTGCCAGTACATCGACCTAGACAAAGGGTCCGGAAGGAGAACT  
 GCAAAT**AGGGAGGCCCTGGCTCTGGCTGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC**  
 CTCGGGGCATCTCCTGATGCTCCGGGCTCACCCCCCTCCAGCGGCTGGTCCCGCTTCC  
 GGAATTGGCCTGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGCTTGGTGGC  
 AGCATAGCCCCACCCCTGCCCTTGCCTCACGGTGGCCCTGCCACCCCTGGCACACC  
 AAAATCCCAC TGATGCCCATCATGCCCTCAGACCCCTCTGGCTCTGCCCTGGGGCCTG  
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAACTGGGTCA GCCTCA  
 GGGCAGGAGTCCCACCTCCAGGGCTCTGCTCGTCCGGGCTGGGAGATGTTCTGGAGGA  
 GGACACTCCCAC TAGAACCTGGCAGCCTGAAGTTGGGTCA GCCTCGCAGGAGTCCCAC  
 CCTCCTGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCAACCATGTGGACTCCAG  
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTGAATGCCAGCCCTGCTCCTCTGTGTTG  
 CTTGGGCCACCTGGGCTGCACCCCTGCCCTTCTGCCCTACCCCTACCTAGCCTTG  
 CTCTCAGCCACCTTGATAGTCACTGGCTCCCTGTGACTTCTGACCCCTGACACCCCTCC  
 GGACTCTGCCCTGGCTGGAGTCTAGGGCTGGGCTACATTGGCTTCTGACTGGCTGAGGA  
 CAGGGGAGGGAGTGAAGTTGGTTGGGTGCCACTCTCAGCACCCACATTT  
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAGTCCCCATCTGATTAAAAAA  
 AAAAAA

## FIGURE 46

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTGPPAT
PAYWDGEKEVLA VARGAPALLTCVNRGHVWTDRHVEEAQQVVHWDRQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIEPLEVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEP PPRGSPGNSSHSGAPGPDTLARGHNVINVIPESRAHFFQQLGYVLATL
LLFILLLVTLAARRRRGGYEYSDQKSGKSKGDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDL DKGFRKENCK
```

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

## FIGURE 47

CGCCGGAGGCAGCGCGCGTGGCGCAGCGCGAC**ATGGCCGTTGTCAGAGGACGACTTT**  
 CAGCACAGTCAAACCTCACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
 ACTGCTTGAGAAGCTGCTGGACCGCCGCCCTGGCCTGCAGAGGCCGAGGACCGCTTCT  
 GTGGCACATACATCATCTTCTTCAGCCTGGCATTGGCAGTCTACTGCCATGGAACCTCTT  
 ATCACTGCCAAGGAGTACTGGATGTTCAAACACTCCGCAACTCCTCCAGGCCAGCCACCGGGGA  
 GGACCCCTGAGGGCTCAGACATCCTGAACACTTTGAGAGCTACCTTGCCTGCCGTTGCCTCCACCG  
 TGCCCTCATGCTGTGCCTGGCCAACCTCCTGCTTGTCAACAGGGTTGCAGTCACATC  
 CGTGTCCCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACGGTGA  
 GGTGGACACTTCCTCCTGGACCCGTGGTTTTTGCGGTCACCATTGTCTGCATGGTGATCC  
 TCAGCGGTGCCCTCACTGTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTCCATG  
 AGGAACCTCCAAGCAGCAGTGAATACAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC  
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTGACGG  
 CCACCATCTCCTCGTCTGCATGGACTCTACCTGCTGCTGCCAGGCTGGAGTATGCC  
 AGGTACTACATGAGGCCTGTTCTTGGGCCATGTGTTCTGGTGAAGAGGAGCTCCCCA  
 GGACTCCCTCAGTGCCTCGGTGGCCTCCAGATTCAATTGATTCCCACACACCCCCCTCTCC  
 GCCCCATCCTGAAGAAGACGGCCAGCCTGGCTCTGTGTCACCTACGTCTTCCATCACC  
 AGCCTCATCACCCGCCGTGCAACCAACATCGAGTCCTCAACAAGGGCTGGGCTCACT  
 GTGGACCACCAAGTTTCATCCCCCTCACTACCTTCCCTGTACAACATTGCTGACCTAT  
 GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCAACAGCAAGGCGCTCCAGGG  
 TTCGTGCTCTCGGACCTGCTCATCCCCCTTCTCGTGTCTGTAACCTACAGCCCCCGT  
 CCACCTGAAGACTGTGGTCTTCCAGTCGATGTGACCCGCACTCCTCAGCTCCCTGCTGG  
 GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCTACGGGCTAAGATTGTGCCAGG  
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTATGTGTGCTGGGCTAACACTGGG  
 CTCAGCCTGCTCACCCCTGGTCACCTCATC**TAGAAGGGAGGACACAAGGACATTGGTG**  
 CTTCAAGAGCCTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC  
 TAAAGTTCACTGGGGACAGAGAGCAGACACTCGGGCTCATCCCTCCAAGATGCCA  
 GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCATATAACAGAACACT  
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGTACTCCCTCACAGCTGATGGTTA  
 ACATTCCACCTTCTTCTAGCCCTCAAAGATGCTGCCAGTGTGCGCCCTAGAGTTATTACA  
 AAGCCAGTGCCAAACCCAGCCATGGCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCT  
 GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCATTACCTGAAGGGTCTCCCTGGAATGGA  
 AGTCCCCTGGCATGGTCAGTCCTCAGGCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
 GCGGGTGAACAACTGCCACTAACAGAGACTGGAAAACCCAGAAAGATGGGCTTCCATGAAT  
 GCTCATTCCAGAGGGACCAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG  
 TTTCAAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGCTAAGATGAGGGTC  
 TTTCAGTGTTCCTGTTACAACATGTCAAAGCATTGGTTCAAGGGCGTAATAAAACTTGC  
 GTATTCAAAA

## **FIGURE 48**

MAVVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGLQRPEDRFCGTYIIFFSLGI  
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
LVNRVAVHIRVLASLTIVLAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI  
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY  
LLLSRLEYARYYMRPVLAAHVFSGEELPQDLSAPSVASRFIDSHTPPLRPILKKTASLGF  
CVTYVFFITSЛИYPAVCTNIESLNKGSGSLWTTKFFIPLTFLLYNFADLCGRQLTAWIQVP  
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSLLGLSNGYLSTLAL  
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
305-330, 448-472

## FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTCACCAAGAGCTGGAGACACCA  
 TCTCCCACCGAGAGTC**ATG**CCCCATTGGCCCTGCACCTCCTCGCCTCGTCCCCATCCTCC  
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTCGAGAAATGC  
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTACCTGGGGCTCAATCGGACCT  
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGCCGGCTGGTGGCCGCCAAGGTGC  
 TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGCCGCATC  
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGGCCATGCGCATGCCAG  
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGCTCAACCTGACCAAGTTCACCC  
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG  
 AAGGTGCCCGAGAAGCTGGCTACGCCCTGCGTCCCCAGGAAAAGGCCACTGCCCGAAGA  
 CATCTACCAAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGACTGGGCTGCAGAAAGG  
 CGATGAAGAAGTTGAAAGGCACACGCTCTTGAATATCTCTGGGGAGGGAACCTGAGC  
 CGGCCGGCCGTGCAGCTCTGGAGACGTGATGTCCGAGGATGGCTTCTTATCTCAGCTT  
 CGCCGAGGCCCTCCGGGCCACAGCTGCCCTAGCGACAGACTCCAGTACAGCCGCATCGTGG  
 GTGGCTGGACCTGCTGCCCGCGCTGCTGAGCTCGCTGTCCGGCTTGTGCTGTTGAAC  
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC  
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG  
 CGGTGAAGCGCATCACCTCTGCCGCCGCTGCCCGCACATGCAGGAGGCGCTGCCGGAGG  
 CTGCACTACGTGCCGCCACCAAGGTGTTCTAACGCTTCCGAGGCCCTCTGGCGCGAGGA  
 GCACATTGAAGGCCGCACTCAAACACCGATGCCCGTGCATGATTTCTACCCGCCGC  
 CGCGCAGGGCGCGCTGCTGGCTCGTACACGTGGTGGACGCCGGCAGCGTGGCGATTGCACGGGCC  
 GGCTTGAGCCGGGAAGAGGCCTTGCCTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC  
 TGTCGTGCCAGCTCTGGACGGCACCGCGTGTCAAGCGTTGGCGAGGACAGCACA  
 GCCAGGGTGGCTTGTGGTACAGCCGCCGGCTCTGGCAAACCGAAAAGGATGACTGGACG  
 GTCCCTTATGCCGCATCTACTTGCCTGGCGAGCACCCGCCTACCCGCACGGCTGGTGG  
 GACGGCGGTCAAGTCGGCGCTGCCGCCATCAAGATCAACAGCCGAAGGGCCTGCAT  
 CGGACACGCCAGCCCCGAGGGCACGCATCTGACATGGAGGGCAGGGCATGTGCATGG  
 GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGG  
 CCAGTTATCTCTCCAAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTTCGGAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 50**

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLSAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRII  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVEKLGYALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGLNSRPAVQLLGDVMSEDGFFYLSFAEALR  
AHSCLSDRQLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPARNL  
KVLKADVVLLTASGPRAVKRITFSPPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG  
HSNTDRPSRMIFYPPPREGALLLASYTWSAAAAFAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIVFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

## FIGURE 51

CTGACATGGCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGCCCTCTGCCTGC**AT**  
**G**ACGCTCTGAAGCCACCCCTGTCTCTGGAGGAACCACAGAGCAGGGAAAGGACAGGGACTCGTGTGGCAGGAA  
 GAACTCAGAGCCGGGAAGCCCCCATCACTAGAAGCACTGAGAGATGGGGCCCTCGCAGGGCTGAATTTCCT  
 GCTGCTGTTACAAAGATGCTTTATCTTAACTTTGTTCCCCTCGCAGGGCTGAATTTCCT  
 CCTGACATTTGGAGCTGCCATCTCTGTGGCTGATCACAGACCTCAACCCGCTTACCTCTTGACCTGAA  
 CAATCAGTCTGTGGATTGAGGGAGGAGCACCGAAGGGGTTCCAGAAGAACAAATGACCTAACAGTGTG  
 CTTCTCAGATGCCAACAGACTATGTATGAGGTTTCCAAGAGGACTCGCTGTGCTGACAATGGGCCCTGCTGG  
 ATATAGAAAACCAACCAGCCCTACAGATGGCTATCTTACAAACAGGTGCTGATAGAGCAGAGTACCTGGGTT  
 CTGCTCTTGATAAAGGTTATAATCATCACAGACAGGTTGTCGGCATCTTGTCTCAGAATAGGCCAGAGTG  
 GATCATCTCCGAAATTGGCTTGTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAC  
 CATCGTACATATTGTCAACAAGGCTGATATGCCATGGTGTGACACACCCAAAAGGCATTGGTGTGAT  
 AGGAATGTAGAGAAAGGCTTCACCCCGAGCCTGAAGGGTGTACATCCTTATGGACCCCTTGATGATGACCTGAA  
 GCAAAGAGGGAGAAGAGTGAATTGAGATCTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCAG  
 AAAACCTGTGCCCTCTAGCCCAGAACAGACCTGAGCGTCATCTGCTCACAGTGGGACCACAGGTGACCCAAAGG  
 AGCCATGATAACCCATCAAATATTGTTCAAATGCTGCTGCCCTCTCAAATGTGTGGAGCATGCTTATGAGCC  
 CACTCCTGATGATGTGCCATATCCTACCTCCCTGGCTCATATGTTGAGAGGATTGTACAGGCTGTTGTGTA  
 CAGCTGTGGAGCCAGAGTTGGATTCTCCAAGGGATATTGGTTGCTGGCTGACGACATGAAGACTTGAAGCC  
 CACATTGTTCCCGCGGTGCCCTGACTCTTAACAGGATCTACGATAAGGTACAAATGAGGCAAGAACACCC  
 GAAGAAGTTCTGTTGAAGCTGGCTGTTCCAGTAAATCAAAGAGCTCAAAAGGGTATCATCAGGCATGATAG  
 TTTCTGGGACAAGCTCATCTTGCAAAGATCCAGGACAGGCTGGGCGGAAGGGTTGTTGAATTGTCAGTGGG  
 TGCCCATGTCCACTTCAGTCATGACATTCTCCGGGAGCAATGGGATGTCAGGTGTTGAAGCTTATGGTCA  
 AACAGAATGCAAGGTGGCTGTACATTACATTACCTGGGACTGGACATCAGGTGACCTGGGGTGGCCCTGGC  
 TTGCAATTACGTGAAGCTGGAGATGTGGCTGACATGAACACTTTACAGTGAATAATGAGGAGAGGTCTGCAT  
 CAAGGGTACAAACGTTCAAAGGATACCTGAAGGACCCCTGAGAACAGACACAGGAAGCCCTGGACACTGATGGCTG  
 GCTTCACACAGGAGACATTGGTCGCTGGCTCCGAATGGAACTCTGAAGATCATGACCGTAAAAAGAACATT  
 CAAGCTGGCCAAGGAGAATACATTGACCCAGAGAAGATGAAAGAACATCTACAACAGGAGTCACCAGTGT  
 AATTTTGACACGGGGAGAGCTACGGTCATCTTAGTAGGAGTGGTTCTGACACAGATGTTACCTCC  
 ATTGCAAGCTGGGCTGAGGGCTCCTTGAGGAACGGTGTGACAAACAGTTGTAAGGGAGCCATT  
 AGAAGACTTGCAAGAAAATTGGAAAGAAAGTGGCTTAAACTTTGAACAGGTCAAAGCCATTTCATCC  
 AGAGCCATTTCATTGAAAATGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTCAAATACT  
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGCCACTG  
 TGCACTGCTGTGAGAAAATGGATTAAAAACTATTCTACATTGTTGCTTCTCCTATTTTTTAAC  
 TGTTAAACTCTAAAGCCATAGCTTGTGTTTATATTGAGACATATAATGTGAAACTTAGTCCAAATAATCA  
 ATCCTGCTTCCATCTCGATGTTGCTAATATTAAAGGTTCAAGGCTACTTTATCAACATGCCTGTCTCAA  
 GATCCCAGTTATGTTCTGTGCTCTCATGATTCCAACCTTAATACTATTAGTAACCCACAAGTTCAAGGGT  
 CAAAGGGACCCCTGTGCCCTCTTGTGATAAACATAACTGCCAACAGTCTATGCTTATTAC  
 TCTCTACTGTCAAACTAAGAGATTAAATTCTGAAAAGTCTGCTTACATTCACTGTTCTAGCCACTCCAC  
 AAACCACTAAAATTGTTAGCTTACACTCATGTCATCATATCTATGAGAACATGTCCTCGATGCTCTT  
 CTGCGTAAATTGTTAGCTGACTGAAGGGAAAAGTTGATCATACCAAAACATTCTCAAACCTCTAGTTAGATA  
 TCTGACTTGGAGTATTAAAATTGGGTCTATGACATACTGTGCTGAGCTGGAAAGCTGTTCTAAAGCATTATT  
 CAGTAGGAACGGGGACTAAATCTGTTCCCTACAGTTGCTGAGCTGGAAAGCTGTTGGGGAGAGTTGACA  
 GGTGGGCCAGTGAACCTTCCAGTAAATGAAGCAAGCAACTGAATAAAAACCTCTGAACTGGGAACAAAGATCT  
 ACAGGCAAGCAAGATGCCACACAAACAGGCTTATTCTGTAAGGAAACCAACTGATCTCCCCCACCTGGATT  
 AGAGTTCTGCTCTACCTAACCCACAGATAACACATGTTGTTCTACTTGTAAAGTCTTAAATAAAC  
 TATTACAGATAAAAAAA

**FIGURE 52**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775  
 <subunit 1 of 1, 739 aa, 1 stop  
 <MW: 82263, pI: 7.55, NX(S/T): 3  
 MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN  
 FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARKGVSQKNNDLTS  
 CCFSDAKTMYEVQTRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS  
 PDQFVGIFQAQNRPWEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL  
 VLIGNVEKGFTPSSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED  
 LSVICFTSGTTGDPKGAMITHQNIVSNAAAFLKCVEHAYEPTPDDVAISYPLAHMFERIVQ  
 AVVYSCGARVGFFQGDIRLLADDMKTILKPTLFPAPRLLNRIYDKVQNEAKTPLKKFLLKLA  
 VSSKFKELOKGIIRHDSFWDKLIFAKIQDSLGGRVRVIVTGAAPMSTSVMFFRAAMGCQVY  
 EAYGQTECTGGCTFTLPGDWTSGHGVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK  
 GYLKDPEKTQEALDSGWLHTGDIGRWLPGNTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR  
 SQPVLQIFVHGESLRSSLGVVVVPDTDVLPSFAAKLGVKGSFEELCQNQVVRRAILEDLQKI  
 GKESGLKTFEQVKAIFLHPEPFSIENGLLPTLAKRGELSKYFRTQIDSILYEHIQD

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

## FIGURE 53

GGAGGC GGAGGCCGCGCGAGCCGGCGAGCAGT GAGGGCC TAGCGGGGCC GAGCGGGG  
 CCCGGGGCCCTAAGCCATT CCTGAAGTCATGGCTGGCAGGACATTGGTGACCCGCAAT  
 CCGGT **ATG** GACGACTGGAAGCCCAGCCCCCTCATCAAGCCCTTGGGCTCGGAAGAAGCGG  
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGC GGAGATTCTGTCA  
 GACAGGGGCCGTGCTTTCCCTGCTGGTACTGTCATTGTCAATATCAAGTGATCCTGGACA  
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC  
 CTAGGCCGCTGGAGCCCCACGGCGAGAGCAGTGGTCCCCGGCTGGACGTAGA  
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACTGGTGTGGAGGATG  
 AGGCCGGGAGCAGGGCCGGGCATCCATGTCATTGTCCTCAACCAGGCCACGGCACGTG  
 ATGGCAAAACGTGTGTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCT  
 CAACATGGTAGGCCCGGCCAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTCCACC  
 TCAAGGACACAGCCAAGGCTGCTGAGGAGCCTGGCAGGCCAGGCTGCCCTGGGC  
 TGGAGGGACACATGGGCCTCGTGGGACGAAAAGGAGGTCTGTCTCGGGGAGAACATTC  
 TAAGTCACCTGCCCTCTTCTGGGGGACCCAGTCTGCTGAAGACAGATGTGCCATTGA  
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGCAGACACAGAGCTGAACCGTCGCCCGGC  
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCATCGA  
 GTTCAGCCCTGACCCACTCCCAGACAACAAGGTCTCAATGTGCTGTGGCTGTCTCAG  
 GGAACCGACCCATTACCTGTACAGGATGCTGCCCTCTGCTTCAAGCCCAGGGGTGTCT  
 CCTCAGATGATAACAGTTTCAATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT  
 GTTGGTCTGAGGGGCATCCAGCATACTCCCATTGACATCAAGAATGCCCGTGTCTCAGC  
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTCCGGAGGCCAAGTTGCTGTGGTT  
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTCAGTTCTGAGCCAATCCATCCACCT  
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTGCCTGGAATGACCAGGGGTATGAACACA  
 CGGCTGAGGACCCAGCACTGTACCGTGTGGAGACCATGCCTGGCTGGCTGGGTGCTC  
 AGGAGGTCTGTACAAGGAGGAGCTTGAGCCAAGTGGCTACACCGAAAAGCTCTGGGA  
 TTGGGACATGTGGATGCGGATGCCCTGAACAAACGCCGGGCCAGAGTGCATCATCCCTGACG  
 TTTCCGATCCTACCACTTGGCATGTCGGCTCAACATGAATGGCTACTTCAACGAGGCC  
 TACTTCAGAAGCACAAGTTCAACACGGTTCCAGGTGTCAGCTCAGGAATGTGGACAGTCT  
 GAAGAAAGAAGCTTATGAAGTGGAAAGTTCAAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC  
 ACAGCAAGAACCCCTGTGAAGACTCTTCCTGCCAGACACAGAGGGCCACACCTACGTGGCC  
 TTTATTGAGAAGAGATGACTTCACCACCTGGACCCAGCTGCCAAGTGCCTCCA  
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCTGTGGAGATTGTTGGAAAGAAGA  
 ACCACTTCTGGTGGTGGGGTCCCAGCTCCCTACTCAGTGAAGAACCCACCCCTCAGTC  
 ACCCCAAATTCTGGAGCCACCCCCAAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC  
**ATG** GACCTCCTCCAGGACCCCTGCAGGGCTGGTACTGTGTAACCCAGGCTGGCTAGCCCT  
 TCCCTCCATCCTGTAGGATTTGTAGATGCTGGTAGGGCTGGCTACCTTGTGTTTAACA  
 TGAGACTTAATTACTCAAGGGAGGGTCCCTGCTCCAACACCCGTTCTGAGTT  
 AAAAGTCTATTATTACTTCCCTGTTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG  
 ATCCCTAGCAGCTCATCCTGCCCTTGAATACCCCTCACTTCCAGGCCTGGCTCAGAATCTA  
 ACCTATTATTGACTGTCCTGAGGGCCTGGAAAACAGGCCGAACCTGGAGGGCCTGGATTTC  
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGCTGGCTTACTCAGGAAACTGCTGTGCC  
 CAACCCATGGACAGGCCAGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCCTA  
 GACACTGGGACCAAGGCCCTCTCAGCCTCTTGTCCAGATTCAAAGCTGGATAAGTT  
 GGTCAATTGATTAAGGAGAAGCCCTGGGAAAAA

## **FIGURE 54**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPDRVLDVEVYSSRSKVVAVDGTIVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRRRFCSKVEGYGSVCSCDKPTPIEFSPDPLPDNKVLNVPAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGVLRRLSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSDLKKEAYEVEVHRLLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

## FIGURE 55

CGGACGCGTGGCTGGTGGGAAGGCCAAAGAACTGGAAAGCCCCTCTGGAACCCACAC  
 CTGTTAAAGAACCTAACGACCAATTAAAGCCACTGGAAATTGTTGCTAGTGGTGTGGGTGAATA  
 AAGGAGGGCAGA**ATG**GATTTCATCTCATTAGCCTGCTGCTCTGGCTATGTTGGTGGGTGAATA  
 CGTGGCCGGAATCATTCCCTGGCTGTTAATTCTCAGAGGAACGACTGAAGCTGGTACTGTTGG  
 GTGCTGGCCTCTCTGGAACTGCTCTGGCAGTCATCGCCTGAAGGAGTACATGCCCTTATGAA  
 GATATTCTTGAGGGAAAACACCAAGCAAGTGAACACACATAATGTGATTGCATCAGACAAAGCAGC  
 AGAAAAATCAGTTGTCATGAACATGAGCACAGCCACGACCACACAGCTGCATGCCTATATTGGTG  
 TTCCCTCGTTCTGGGCTCGTTCATGTTGCTGGTGGACCAGATTGTAACCTCCATGTGCATTCT  
 ACTGACGATCCAGAACAGCAGCAAGGTCTAGCAATTCAAATCACCACACAGCTGGTCTGGTGTCCA  
 TGCTGCAGCTGATGGTGTGTTGCTTGGGACGAGCAGCATCTACCTCACAGACCAGTGTCCAGTTAATTG  
 TGTTGTGGCAATCATGCTACATAAGGCACAGCAGCTGCTTGGACTGGTTCTTCTTGATGCATGCT  
 GGCTTAGAGCGGAATCGAATCAGAAAGCAGCTGCTGGTCTTGATGGCAGCACAGTTATGTCCAT  
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAACGCCCTTCAGAGGTGAACGCCACGGAGTGG  
 CCATGCTTTCTGCGGGACATTCTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGGGCGGA  
 ATAGGGCACAGCCACAAGCCCGATGCCACAGGGAGGGAGAGGCCTCAGCCGCTGGAAGTGGCAGCCCT  
 GGTTCTGGGTTGCCTCATCCCTCATCCTGTCAGTAGGACACCAGCAT**TAA**ATGTTCAAGGTCCAGC  
 CTTGGTCCAGGGCCGTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTCCTCAGTC  
 TCTGTCTCACCTGCGCATCTACATGTATTCTAGAGTCAGAGGGAGGTGAGGTTAAAACCTG  
 AGTAATGGAAAAGCTTTAGAGTAGAAACACATTACGTTGCAAGTCTAGACATCCATTGTGT  
 TATCTTTAAAAGGCCCTGACATTTCGCTTTAATATTCTCTTAACCTATTCTCAGGGAAAGATG  
 GAATTAGTTAAGGAAAAGAGGAGAACCTCATACTCACAATGAAATAGTGATTATGAAAATACAGT  
 GTTCTGTAATTAAGCTATGTCCTTCTTAGTTAGAGGCTCTGCTACTTATCCATTGATTTT  
 AACATGGTTCCCACCATGTAAGACTGGTGCTTAGCATCTATGCCACATGCGTTGATGGAAGGTATA  
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGTGAGGAAAATGATAGC  
 AAAGACACATTGAAAGCTCTTATACTCAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT  
 TAAACAGCTCCTTGGCACGTGCCCTCTGAATCCAGCCTGCATTCCATCAAATGGAGCAGGAGG  
 TGGGAGGAGCTCTAAAGAGGTGACTGGTATTGTAGCATTCTGTCAGTTCTCAGGCTTCTCAAGAA  
 ACCTGTCACATTCTAGAGAGGAGCAAGTCTAGTAGTTCTAGTTGATTTGGATGGTTAT  
 CAGTCAGATCACAAAGTCTTGGAAATTAGGATATTAAATTAAAGTGTGATTTGGATGGTTAT  
 TGATATCTTGTAGTAGCTTTTAAAGACTACCAAAATGATGGTGTCTTTTTGGATGGTTAT  
 TTTTTTTAATTATTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTGAGCTTT  
 GGCGACACTGTCCTCTCACATAACCACCTGTCAGCAAGATGGATCATAAAATGAGAAGTGGCTA  
 TTGATTAAAGCTTATTGAAATCATGTCCTGTCCTCGCTCTTGTCTTTCTTAACCTT  
 TCCCTCTAGCCTCTCGCCACAATTGCTGCTACTGCTGGTGTAAATATTGTGTGGATGAATT  
 CTTATCAGGACAACCACTCTCGAAGTAAATGAAGATAATAATCTTATCTTATCCCCTT  
 CAAAGAAATTACCTTGTGTCAAATGCCCTTGTGAGGCCCTAAACACCCCTCATGTGAA  
 ATTGACACAATCACTAATCTGGTAAATTAAACAATTGAGATAGCAAAAGTGTAAACAGACTAGGATA  
 ATTGTTTTCATATTGCCAAATTGTAACACCTGTCTGTCATTAAGTGTATAATTGTAT  
 TATAATTATTCTACCTACCATTCAAAACACATTACACTAAGGGGGAAACCAAGACTAGT  
 TCTCAGGGCAGTGGACGTAGTAGTTGTAACACCTGTTCTATGACGCAAGCTAGCATGCCTATG  
 ATTGTTCTCATGAATTGCACTGGATCAGCAGCTGTGGAAATAAGCTGTGAGGCCCTGT  
 GGCCACAGTGGAGGAAAGTAGCACAATAGGATACAGTGTATGAGTCATTGGCAACAATTGCA  
 ATTGTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTCCTGATTGGATGTTAACAGCT  
 GACTGGTGTGAGACTTGAGGTTCATCTAGTCCTCAAAACTATATGGTGCCTAGATTCTCTGGA  
 AACTGACTTGTCAAATGAGATTGTAGTGTCAAAAAAAA

## **FIGURE 56**

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ  
IGNSHVHSTDDPEAARSSNSKITTTLGLVVHAAADGVALGAAASTSQTSQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKHLLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILIISVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

## FIGURE 57

GCTCGAGGCCGGCGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCGGATCCC  
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTGAGATGATGGGCTTGG  
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGTGGCCGCCCTGGTGGCCTGCATC  
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCGGAGCGTGGACCTCCAGACACGGAT  
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGCGCCGTGGAGCTGAAGA  
 AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCAGGGAGCAGCTTGACAAAATCCAGTCCAGC  
 CACAACTTCCAGCTGGAGAGCGTCAGAACAGCTGTACCAAGGACGAAAAGGCGGTTTGGTGA  
 TAACATCACACAGGTGAGAGGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCCTGCAGA  
 GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTCAGAAGAACAGACCAACCTGGAG  
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
 TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCAGAGACCTGA  
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
 GCAGCAGGCCCTGCCACACACAGAGGTGCCACAAGGGAAACGTGCTGGTAACAGCAA  
 GTCCCAGACACCAGCCCCCAGTTCCGAAGTGGTTGGATTCAAAGAGACAAAGTTGAGAAAG  
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG  
 CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAAGAGGCTCGGGGAGCCGG  
 AGAACTGGGCCAGACCCCACAGGTGCAGGCTGCCCTGTCACTGAGCCAGGAAAATCCAGAGA  
 TGGAGGGCCCTGAGCGAGACCAGCTTGTCACTCCCGACGGACAGGAGGAGCAGGAAGCT  
 GCCGGGGAGGGAGAAACCAGCAGAAACTGAGAGGGAGAAGATGACTACAACATGGATGAAAA  
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAAGCAGCCCTGGCAGGGAAATGACAGAAACATAGATG  
 TTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTACTTGATCAGCGTGAAAAGCGG  
 AATCATAACACTCTGAATTGAACTGGAATCACATATTCACAAACAGGGCGAAGAGATGACTA  
 TAAAATGTTCATGAGGGACTGAATACTGAAAATGTACTAAATAATGTACATCTGA

## **FIGURE 58**

MMGLGNGRRSMKSPPPLVLAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERGA  
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL  
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSENNNDQRQQQLQALSEPQPRLQAAGLPHTEVPGKGNVLGNSKSQTPAPSSEVVLDSKR  
QVEKEETNEIQVVNEEPQRDRLPQEPMREQVVEDRPVGGRGF GGAGELGQT PQVQAALSVSQ  
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNMDENEAESETDKQAALAGND  
RNIDVFNVEDQKRDTINLLDQREKRNHTL

**Signal peptide:**

amino acids 1-29

## FIGURE 59

**GGATGCAGAAAGCCTCAGTGGCTTCCCTGGCCTGGGCTGCTTCCCTTCTACGCTGGCATTGCCCTTTCA**  
**CCAGTGGCTTCCCTGCTCACCCGTTGGAGCTCACCAACCATAAGCAGCTGCCAAGAGCCCCCAGGCCCTGGGCTCC**  
**TGCCATGGGGAGCCAAGGGAAACCTGGGCCCTGCTGGATGGCTTCCCGATTTCGGGGGTGTTGGTGTGCTGA**  
**TAGATGCTCTGCGATTGACTTCGCCAGCCCCAGCATTACAGTGCCTAGAGAGCCTCTGTCTCCCTACCCCT**  
**TCCTGGCAAACTAAGCTCCTTGCAAGGAGATCTGGAGATTCAAGCCCCACCATGCCGGCTTACCGATCTCAGG**  
**TTGACCCCTCCTACCACCAACATGCAGCGCTCAAGGCCCTCACCACTGGCTACTGCCTACCTTATTGATGCTG**  
**GTAGTAACCTGCCAGCCACGCCATAGTGGAAAGACAATCTCATTAAGCAGCTCACCACTGCAGGAAGGCGTAG**  
**TCTTCATGGGAGATGATACTGGAAAGACCTTTCCTGGTCTTCTCAAAGCTTCTTCCCATCCTCA**  
**ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAAACACCTTACCCACCATGGACAGTGGTGAATGGG**  
**ACGTGCTGATTGCTCACTCCTGGGTGTTGGACACTGTGCCACAAGCATTGGCCCTCACCAACCTGAAATGCCA**  
**AGAAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG**  
**CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGACAGTGGAGCTGGAGGTCTCAGCTGCTCTTTC**  
**TGTATAGCCCCACAGCAGTCTTCCCAGCACCCACAGAGGGACAGGGTGAATTCTCAAGTTAGCCTGTG**  
**CCACGCTGGCCCTGCTGGCCCTGCCATCCCATTGGGAATATGGGGAAAGTGTGATGGTGAAGCTATTCTCAG**  
**GGGGTAGGGACTCCCAGGCCACTCCTCTGCTTAGGCCAACGCTCAGCTCTCCATCTCAATGCTCAGCAGGTG**  
**CCCGATTCTCATACCTACTCAGCTGACTCAGGACCTCAAGCTAAGGAGCTCATCAGCTGAGAACCTCT**  
**TCTCCAAGGCCCTGCTGACTACCAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA**  
**TTGCTGAGCTGCACTGAGTTCTGCGGGAGCTGGCCATGTGCATCGAGTCTGGCTCGTTCTCTGGTCC**  
**GCATGGCGGGGGTACTGCTCTTGGCTGCTTATCTGCTGCTGGCATCTCAGTGGCAATATCCC**  
**CAGGCTTCCATTCTGCCCTACTCTGACACCTGTGGCTGGGCTGGTTGGGCCATAGCGTATGCTGGAC**  
**TCCCTGGGAACTATTGAGCTGAAGCTAGATCTAGTGTCTTAGGGGCTGTGGCTGAGCTCATTCTCCCTT**  
**TTCTGTGGAAAGCCTGGCTGGCTGGGCTTCAAGAGGCCCTGGCAACCCCTGTTCCCATCCCTGGGCCGTCC**  
**TGTTACTCCTGCTGTTGGCTGTGTTCTCTGTATAGTTGGTAGCTGAGGCCAGGGCACCCCT**  
**TCCTTTGGGCTCATCATCCTGCTCTGGTTGGCAGCTTACTGGGAGGGCAGCTGCTCCACCTAAGCTAC**  
**TCACAATGCCCGCCTGGCACTTGCACAAACAAACCCCCACGGCACAATGGTCATATGCCCTGAGGCTTG**  
**GAATTGGGTTGCTTTATGTACAAGGCTAGCTGGCTTTTACATGGTGAAGAGACACCTGTTGCCACT**  
**CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGCGAGCAAGAATTATGGTATGGAGCTGTGTGG**  
**CGCGCTGGTGCCCTGTTAGCTGCCGTGCGCTTGTGGCTCGCCGTATGGTAATCTCAAGAGCCCCGAGCCAC**  
**CCATGCTTTGTGCGCTGGGACTGCCCCATAATGGCATTGGTACTGCTGCCTACTGGCATTGGCTCGGGGG**  
**CAGATGAGGCTCCCCCGCTCCGGGTCTGGGTCTCTGGGCATCCATGGTGTGCCTCGGCTGGGTGTAGCAGGGC**  
**TGGCTGCTTCAGGGCTCCGCTGCTGACAGTGTGGTAAGGCTGGGCAGGGCTCCAA**  
**GGACCAGGACTGTCCCTACTCCCTTCAGGCCCTTCACTCTCAAGCTGACTGGATTATGGTGTCCCTCAA**  
**TCTACCGACACATGCAGGAGGAGTCCGGGCCGGTTAGAGAGGACAAATCTAGGGTCCCCTGACTGTGGCTG**  
**CTTATCAGTTGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTACCCCTGTTGGCTTCCCACCTCTGCTG**  
**TGCATGCGAGCGCATCAGCCTGTGTTCTGCTTCTGAGCTTCCCTACATCTGCTTGCTG**  
**CTGGGATACCGTCACCAACCCCTGGCCTTTACTGTGCATGGCAGGCTCGGCTGGGCCCTCATGGCCA**  
**CACAGACCTCTACTCCACAGGCCACCAGCCTGCTTCCAGCCATCCATTGGCATGCAAGCCTCGTGGGATTCC**  
**CAGAGGGCATGGCTCTGTACTTGGCTGCCCTGGCTACTGAGGAGGCAACACCTTGCCTCCCACCTCTCT**  
**TTGCACTAGGGTGGCCACTGCTCTGCTGGCTTCCCTGTGTGAGAGTCAGGGCTGCCAAGAGACAGCAGC**  
**CCCCAGGGAAATGAAGCTGATGCCAGACTCAGACCCGAGGGAGGAAGAGGAGGCCACTGATGGAGATGCCGGG**  
**ATGCCCTCAGCACTCTGAGACTGCTGAGCGTGGCCTCAAGTACCTTTATCCTGGTATTGAGATTGATGGT**  
**TGGCCTGTGCCCTGGCAGCCTCCATCCTCGCAGGCATCTCATGGCTGGAAAGTGTGTTGGCCCTAAGTTCATAT**  
**TTGAGGCTGTGGCTTCATTGTGAGCAGCGTGGACTTCTCTGGGCATAGCTTGGTAGAGAGTGGATGGT**  
**CTGTGAGCTCTGGTTCAGGCAGCTATTCTGGCCAGCAGAGGTAAGCTAGTGTGATTACTGGCATTGGCT**  
**ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATCTGCAAGACAGGCTCAGCCATAC**  
**TCTTAATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATCTATAATTCAAGGACCAAGTGGAGTA**  
**TGATCCCTAACTCCTGATTTGGATGCACTGAGGGACAAGGGGGGGCGGTCTCCAAGTGGAAATAAAATAGGCCG**  
**GCGTGGGTGACTTGCACCTATAATCCAGCACTTGGGAGGCAGAGGTGGAGGATTGCTGGTCCAGGAGTTCA**  
**AGACCAGCCTGTTGAAACATAACAAGACCCGCTCTACTATTAAAAAAAGTCAATAAAATGATAATAT**

**FIGURE 60**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPPGPGSLPWGSQGKPGACW
MASRFSRVVVLVLIDALRFDFAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF
PGAFSKAFFFPSFNVRDLDTVDNGILEHLYPTMDSGEWDLIAHFLGVDHCGHKHGPHPEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAALFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIPGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRLFHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISPGFPFCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVAAYSSFLPFLWKAAGWGSKRPLATLFPPIPGLVLLLFRLA
VFFSDSFVVAEARATPFLGSFILLVVQLHWEGQLLPKLLTMRPLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL
LLHLLAAGIPVTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLCESQGLRKRQQPPGNEADARVRPEEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFILGIQILACALAASILRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLGLIALVMRVDGAVSSWFRQLFLAQQR

```

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271

## FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTGGGGACGGGCAGTCCCTGT  
 GTCTCTGGTGGTTGCCTAAACCTGCAAACATCACCTCTTATCCATCAACATGAAGA**ATGT**  
 CCTACAATGGACTCCACCAGAGGGCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGT  
 CCTGACAGCTCCAGAGAAGTGAAGAGAAATCCAGAAGACCTCCTGTTCCATGCAACAAA  
 TATACTCCAATCTGAAGTATAACGTGTCGTGAATACTAAATCAAACAGAACGTGGTCC  
 CAGTGTGACCAACCACACGCTGGTCTCACCTGGCTGGAGCCGAACACTCTTACTGCGT  
 ACACGTGGAGTCCTCGTCCCAGGGCCCCCTGCCGTGCTCAGCCTCTGAGAAGCAGTGTG  
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTCTGGTATGTTTG  
 CCCATATCTATTACCGTGTTCCTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
 CGTTGGCAAAGAGAAACACCCAGCAAATTGATTGATTGAAATGAATTGACAAAAA  
 GATTCTTGTGCCTGCTGAAAAAAATCGTGATTAACTTATCACCCCTCAATATCTGGATGAT  
 TCTAAAATTCTCATCAGGATATGAGTTACTGGAAAAAGCAGTGATGTATCCAGCCTTAA  
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTAG  
 GGTATGCTCGCATTGATGAAATTGGTACTCTGAAGAAAACACGGAAGGTACTTCT  
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCCGGATAAAACAGTCATTGAATATGA  
 ATATGATGTCAGAACCACTGACATTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTGCAGG  
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTGGCCCG  
 CAAACGTTACAGTACTCATACACCCCTCAGCTCAAGACTTAGACCCCCCTGGCGCAGGAGCA  
 CACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCAGTGGATCCCC  
 AAACCTGGCAGGCTGTATTCCCTCGCTGTCCAGCTCGACCAGGATTCAAGAGGCTGCGAG  
 CCTCTGAGGGGATGGCTCGAGAGGAGGGCTTCTATCTAGACTCTATGAGGAGCCGGC  
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCACTGGAGGAATGGGGT  
 TATATGTGCAGATGGAAAAC**TGA**TGCCAACACTCCTTGCCTTTGTTCTGTGCAAAC  
 AAGTGAGTCACCCCTTGATCCCAGCCATAAAGTACCTGGATGAAAGAAGTTTCCAGT  
 TTGTCAGTGTCTGTGAGAATTACTTATTCTTCTATTCTCATAGCACGTGTGATTG  
 GTTCATGCATGTAGGTCTCTAACATGATGGTGGGCCTCTGGAGTCCAGGGCTGGCCGGT  
 TGTTCTATGCAGAGAAAGCAGTCAATAATGTTGCCAGACTGGGTGCAGAATTATTCAAGG  
 TGGGTGT

## **FIGURE 62**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815  
<subunit 1 of 1, 442 aa, 1 stop  
<MW: 49932, pI: 4.55, NX(S/T): 5  
MSYNGLHQRFKELKLLTLCISIQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ  
QIYSNLKYNVSLNTKSNTWSQCVTNHTLVLWLEPNTLYCVHVESFVPGPPRRAQPSEKQ  
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILIGNEFD  
KRFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKH  
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSL  
QEEVSTQGTLLSQAALAVLGPQTLQYSYTPQLQDLDPLAQEHTDSEEGPEEPSTLVDWD  
PQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEEGLLSRLYEEPAPDRPPGENETYLMQFMEEW  
GLYVQMN

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

## FIGURE 63

CGGACCGCGTGGCGGGACCGCGTGGCGGGACCGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG  
TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGACGTCTCTGCTGACTGTGGCCACCGCCCT  
GATGCTGCCGTGAAGCCCCCGCAGGCTCCTGGGGGCCAGATCATCGGGGCCACGGAG  
TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGCCAACATCACTGCGGA  
GGCTTCCTGCTGCAGCCCCTGGGTGGTCTCGGCCGCCACTGCTCAGGCCACAGAGACCT  
CCGCACTGGCCTGGTGGTCTGGCGCCACGTCTGAGTACTGCGGAGGCCACCCAGCAGG  
TGTGTTGGCATCGATGCTCTCACCAACGCACCCGACTACCACCCATGACCCACGCCAACGAC  
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGCTGCTGAGGCT  
GCCAGGGAGAAGGGCCAGGCCACAGGCCACAGCGGGGACACGGTGCCGGTGGCTGGCTGGGCT  
TCGTGTCTGACTTGGAGGAGCTGCCGCTGGACTGATGGAGGCCAAGGTCCGAGTGTGCTGGAC  
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGAG  
TGGGGACAGCCACAGACGGGCTTCTGCTCGGCCACTCCGGAGGGCCCTGGTGTGAGG  
ACCGGGCTCACGGCCTCGTTCTCGGGCCTCTGGTGCAGGCCACCCAAAGACCCCGAC  
GTGTACACGCAGGTGTCCGCTTGTGGCCTGGATCTGGACGTGGTCTGGCGAGCAGTCC  
CCAGCCGGCCCCCTGCCTGGGACCAACCAGGCCAGGAGAAGGCCTGAGCCACAACCT  
TGCAGGCTGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCACGGG  
AAGCCTGATGTTCAAGGGTTGGGTGGGACGGCAGCGGTGGGACACCCATTCCACATGCA  
AAGGGCAGAAGCAAACCCAGTAAAATGTTAACTGACAAAAAAAAAAAAAAAAGAAA

## **FIGURE 64**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAQIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTMLCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

**Signal peptide:**

amino acids 1-30

## FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCCGACTCCGGACGCCTGACGCCTGA  
 CGCCTGTCCCCGGCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGACCGTAG  
 CAGGCGCCGCCGTGCTGCTCAAGGACTATGTCACCGGTGGGCTGCCCAAGGCCACC  
 ATCCCTGGGAAGACGGTCATCGTACGGCGCCAACACAGGCATCGGAAGCAGACCGCCTT  
 GGAACGGCCAGGAGAGGAGGAAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
 CGGCAGCAAAGGACATCCGCCGGAGACCCCTCAATACCATGTCAACGCCGGCACCTGGAC  
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTGCAGCAAAGATCATTGAAGAGGGAGGAGCAGT  
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCACTGGACCACCGAGGACGGCT  
 TCGAGATGCAGTTGGCGTTAACCAACCTGGGTCACTTCTCTTGACAAACTTGCTGCTGGAC  
 AAGCTGAAAGCCTCAGCCCCTCGCGGATCATCACCTCTCGTCCCTGGCCATGTTGCTGG  
 GCACATAGACTTTGACGACTTGAACGGCAGACAGGAGAAGTATAACACCAAAGCCGCCTACT  
 GCCAGAGCAAGCTGCCATCGCCTTCAACCAAGGAGCTGAGCCGGCGCTGCAAGGCTCT  
 GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGCAGACACACGGG  
 CATCCATGGCTCCACCTCTCCAGCACCAACTCGGGCCATCTCTGGCTGCTGGTCAAGA  
 GCCCGAGCTGGCCGCCAGCCCAGCACATACTGGCCGTGGCGAGGAAGTGGCGGATGTT  
 TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCCGGCCCCGAGGCTGAGGATGAGGA  
 GGTGGCCCGGAGGCTTGGCTGAAAGTGCCGCCTGGTGGCTAGAGGCTCCCTGTGA  
 GGGAGCAGCCCTCCCCAGA**TAA**CCTCTGGAGCAGATTGAAAGCCAGGATGGCGCCTCCAG  
 ACCGAGGACAGCTGCCGCATGCCGCAGCTCCTGGCACTACCTGAGCCGGAGACCCAG  
 GACTGGCGGCCGCATGCCGCAGTAGGTTCTAGGGGGCGGTGCTGCCAGTGGACTGGC  
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTCCGTCTGCTGCTGCCAGCAGGGGAG  
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGCCGAGGAGGAAGGGGCTC  
 TGTGCACTGCAGGCCACGTCAAGGAGAGCCAGCGGTGCCGTGCGGGAGGGTTCCAAGGTGC  
 TCCGTGAAGAGCATGGCAAGTTGTCTGACACTTGGTGGATTCTGGTCCCTGTGGACCT  
 TGTGCATGCATGGCCTCTGAGCCTGGTTCTCAGCAGTGAGATGCTCAGAATAACTG  
 CTGTCCTCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGG  
 GGTGTTGCTGAGGGCTTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCACTCCC  
 GAGTTCAAGGCTCTGCACGGCATGGAGTGGGAACCCCACCAGCTGCTGCTACAGGACCTGGGA  
 TTGCCTGGACTCCCACCTTCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC  
 TTGCTCATT

## **FIGURE 66**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHGHFLLTNLLDKLASPNSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPPELAAQPSTYLAVALADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR
```

**Signal peptide:**

amino acids 1-17

## FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGCCTGGGGCGCGCTGGCGCGCTGCTGGCGGTGCTG  
 GCGCTCGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGCGACACGTTCTCGCGCTGAC  
 CACGTGGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGCTGCTGAGGCAGTACCTGC  
 GCAGGGAGGAGGCGCGGCTGCGGACCTGACTAGATTCTACGACAAGGTACTTCTTGCAT  
 GAGGATTCAACAACCCCTGTGGCTAACCTCTGCTGCATTACTCTCATCAAACGCCGCA  
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG  
 ATGGCTATGAGAAGGTGGAGCAAGACCTCCAGCCTTGAGGACCTTGAGGGAGCAGCAAGG  
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT  
 TCAGAGAGTCAGTGGCTCTGCATCACTGACCTGTACAGCCCCAACGGCTCTTCTCTCA  
 CAGGGATGACTGCTCCAAGTTGGCAAGGTGGCTATGACATGGGGATTATTACCATGCC  
 ATTCCATGGCTGGAGGAGGCTGTCAGTCTCTCCGAGGATCTTACGGAGAGTGGAAAGACAGA  
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTGGCCTTGCTTATTCCGGCAGGAA  
 ATGTTCTGTGCCCTCAGCCTCTCGGGAGTTCTCTACAGCCCAGATAATAAGAGG  
 ATGCCAGGAATGTTGAAATATGAAAGGCTTGGCAGAGAGCCCCAACCGTGGTAGC  
 TGAGGCTGTACCCAGAGGCCAATATACCCCACCTGCAGACCAGAGACACCTACGAGGGC  
 TATGTCAGACCCCTGGGTTCCAGCCCACCTCTACCAAGATCCCTAGCCTCTACTGTTCTAT  
 GAGACCAATTCCAACGCCAACCTGCTGCTCCAGCCCACCGGAAGGGAGGTACCCACCTGGA  
 GCCCTACATTGCTCTACCATGACTCGTCAGTGACTCAGAGGCTCAGAAAATTAGAGAAC  
 TTGCAGAACATGGCTACAGAGGTCACTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG  
 TACCGCATCAGCAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAACTGGTACCCCTCAA  
 CCACCGCATGCTGCCCTCACAGGCCCTGATGTCGGCCTCCCTATGCAGAGTATCTGCAGG  
 TGGTGAACTATGGCATGGAGGACACTATGAGCCTCACTTGACCATGCTACGTACCAAGC  
 AGCCCCCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTATGATCTATGAGCT  
 GGTGGAAAGCTGGAGGAGCCACAGCCTCATCTATGCCAACCTCAGCGTGCCTGTGGTAGGA  
 ATGCAGCACTGTTGGTGGAACCTGCACAGGAGTGGTAAGGGGACAGTGACACACTTCAT  
 GCTGGCTGTCCTGTCCTGGTGGAGATAAGTGGGTGGCCAACAAGTGGATACTGAGTATGG  
 ACAGGAATTCCGCAACCCCTGCAGCTCCAGCCCAGTGAAGACT**TGA**ACTGTTGGCAGAGAGAAC  
 TGGTGGAGTCTGTGGCTTCCAGAGAACGCCAGGAGCCAAAGCTGGGTAGGAGAGGAGAA  
 AGCAGAGCAGCCTCTGGAAAGAACGCCCTGTCAGCTTGCTGTGCCTCGCAAATCAGAGGC  
 AAAGGGAGAGGTTGTTACCAAGGGGACACTGAGAAATGTACATTGATCTGCCCAAGCCACGGAA  
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCCTGAGAGGGAAGTTCTGG  
 AGTCAGATACTCTGTTGGAACAGGACATCTAACAGTCTCAGGTTCGATCAGTGGTC  
 TTTGGCCTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG  
 GGGCTAGCCTGACTCCCAGAACTTAAAGACTTCTCCCCACTGCCTCTGCTGCAGCCCAAG  
 CAGGGAGTGTCCCCCTCCAGAAGCATATCCAGATGAGTGGTACATTATAAGGATTTT  
 TTTAAGTTGAAAACAACCTTCTTTCTTTGTATGATGGTTTAACACAGTCATTAAAA  
 ATGTTATAAATCAAAA

## **FIGURE 68**

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLLGLLRRYLRGEEARL  
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE  
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ  
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS  
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVAEAVIQRPNIPHLQTRDTYEGLCQTLGS  
QPTLYQIPSLYCSYETNSNAYLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG  
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW  
NLHRSGEGDSDLHAGCPVLVGDKWANKWIHEYGQEFRRPCSSPED

**Signal peptide:**

amino acids 1-19

## FIGURE 69

GAGATAGGGAGTCTGGGTTAAGTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG  
 GAAGCCACCAGACTCCACGGTGTGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGCC  
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCGTAACCCGCGCGGGAG  
 CGCCCAGG**ATG**CCGCGCGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC  
 TGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGCCCTGGTCT  
 GTCTGTGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCTTGAAAGTGCCTTCC  
 TGGCTCCAGCCATCATCCTCATCCTCTGGCGTCGTATGTTCATGGTCTCCTTATTGGT  
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTGATGTACATCCTGGAT  
 CTGCCTCATCATGGAGCTCATGGTGGCGTGGTGGCCTTGACCTCCGGAACAGACCATTG  
 ACTTCCTGAACGACAACATTGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA  
 AACATCATGGACTTGTTCAAGAAAAGTTCAAGTGTGTGGCGGGAGGAACCGAGATTG  
 GAGCAAGAACATCAGTACGACACTGCAGTGCAGTGCCTGGACCCCTGGCCTGTGGGTGCCCTACA  
 CCTGCTGCATCAGGAACACGACAGAACAGTTGTCAACACCATGTGTGGCTACAAACTATGAC  
 AAGGAGCGTTCAGTGTGCAGGATGTCATCTACGTGCAGGCTGCACCAACGCCGTGATCAT  
 CTGGTTCATGGACAACACTACACCATCATGGCGTGCATCCTCCTGGCATCCTGCTTCCCCAGT  
 TCCTGGGGGTGCTGCTGACGCGTGTACATCACCCGGTGGAGGACATCATCATGGAGCAC  
 TCTGTCACTGATGGCTCTGGGCCCGGTGCCAAGCCCAGCGTGGAGGGCGCAGGCACGGG  
 ATGCTGCTTGTGCTACCCAAAT**TAG**GGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
 TGGGATAGCACCTCTCAGTCAACATCGTGGGCTGGACAGGGCTGCGGCCCTCTGCCACA  
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCCTGTGTAGGTCCCACGGCCTGCCTC  
 CCCAGGGAGCAGAGCCTGGCCTCCCTAAAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT  
 GCCCACCTGGGCCTGGGAACAAGGCCCTCTTCTCCAGGCCTGGCTACAGGGAGGG  
 GAGCCTGAGGCTTGCTCAGGGCCATTTCATCTGGCAGTGCCTGGCGGTGGTATTCAA  
 GGCAGTTTGTAGCACCTGTAATTGGGAGAGGGAGTGTGCCCCTGGGCCAGGAGGGAAAGG  
 GCATCTGGGAAGGGCAGGAGGGAAAGAGCTGTCATGCAGCCACGCCATGCCAGGTTGGC  
 CTCTCTCAGCCTCCAGGTGCCTTGAGCCCTTGCAAGGGCGCTGCTCCTTGAGCCTA  
 GTTTTTTACGTGATTTGTAACATTCACTTTTGACAGATAACAGGAGTTCTGAC  
 TAATCAAAGCTGGTATTCCCGCATGTCTATTCTGCCCTCCCCAACCAGTTGTTAA  
 TCAAACAATAAAACATGTTGTTGTTAAAAAA

## **FIGURE 70**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYWLKFSLIIYSTVFWLIGALVLSVGIYAEVERQKYKTLESAFLAP
AIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMELEIGGVVALTFRNQTIDFL
NDNIRRGHENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPAGAKPSVEAAGTGCCLCYPN
```

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

## FIGURE 71

GAGGAGCGGGCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA  
 CACCTGGGAAGATGGCCGGCCGTGGACCTTCACCCTCTGTGGTTGCTGGCAGCCACC  
 TTGATCCAAGCCACCCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGA  
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
 TCAGTGCATGCCGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCCTGGTAACACC  
 GTCCTGAAGCACATCATCTGGCTGAAGGTATCACAGCTAACATCCTCCAGCTGCAGGTGAA  
 GCCCTGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
 ACACGCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAAGCCACCATC  
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCCTGGCCTCAGTGACTGTGCCACCAGCCA  
 TGGGAGCCTGCGCATCCAAGTGTATAAGCTCTCCTGGTAACGCCCTAGCTAACGC  
 AGGTATGAACCTCCTAGTGCATCCCTGCCAATCTAGTGAACCAAGCTGTGCCCCGTG  
 ATCGAGGCTCCTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTAAGGTGCCATTTC  
 CCTCAGCATTGACCGTCTGGAGTTGACCTCTGTATCCTGCCATCAAGGGTACACCATT  
 AGCTCTACCTGGGGCCAAGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC  
 TCTGCAGCTCCCTGACAATGCCAACCCCTGGACAACATCCGTTAGCCTCATCGTGAGTCA  
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTCTCCAGAAGAATTCAATGGTCCGTGG  
 ACTCTGTGCTCCTGAGAGTGCCCCTGGCTGAAGTCAAGCATGGGCTGATCAATGAAAAG  
 GCTGCAGATAAGCTGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCGAGTT  
 TTTTATAGACCAAGGCCATGCCAAGGTGCCAACTGATCGTGTGCTGGAAAGTGGTCCCTCCA  
 GTGAAGGCCCTCCGCCCTTGGTCAACCTGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC  
 ACCAAAGGTGACCAACTTAACTCAACTGAAATAACATCAGCTCTGATCGGATCCAGCTGAT  
 GAACTCTGGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
 ACTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAAGATCTGGGTCCCAGTGTGATTGGT  
 AAGGCCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCC  
 AGCCTCCTGTGGAAACCCAGCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG  
 GGAAGGCTGGTCCCAGCTGGAGTATGGGTGTGAGCTATAGACCATCCCTCTGCAAT  
 CAATAAACACTTGCCTGTGAAAAA

## **FIGURE 72**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPVKVIKEKLTQELKDHNATSILQQPLLSAM
REKPAGGIPLGSLVNTVLKHIWLVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTKWFNNSAASLTMPTLDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSLRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEAAESSLTKDALVLTPASLWKPSSPVSQ
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## FIGURE 73

GAGCGAAC**ATG**GCAGCGCGTTGGCGGTTGGTGTCTGTGACCATGGTGGTGGCGCTG  
 CTCATCGTTGCGACGTTCCCTCAGCCTCTGCCAAAGAAAGAAGGAGATGGTGTATCTGA  
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
 AGTCCCGTGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT  
 CTCCAACGTGACATAGACAGTGTGCGTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC  
 AAACTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTGGCCATGGTGGATTGG  
 ATGAAGGCTCTGATGTATTCAGATGCTAACATGAATTGAGCTTACAGGTGCAGGGTTTCAGC  
 TGAGCAGATTGCCCGTGGATGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC  
 CAAATTATGCTGGTCCCCTATGTTGGATTGCTTTGGCTGTTATTGGTGGACTTGTGTAT  
 CCTCGAAGAAGTAATATGGAATTCTCTTTAATAAAACTGGATGGCTTGCAGCTTGTG  
 TTTTGTGCTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACACCATAAGCCC  
 ATAAGAACACACATTGTTCTGTTAATGGTGGAGTACCTTAGGAATGGTGTGGCTGGTATTG  
 TGAAGCTGCTACCTCTGACATGGATATTGAAAGCGAAAGATAATGTGTGGCTGGTATTG  
 GACTTGTGTATTATTCTCAGTTGGATGCTCTATTAGATCTAAATATCATGGCTAC  
 CCATACAGCTTCTGATGAGT**TAA**AAAGGTCCCAGAGATATAGACACTGGAGTACTGGAA  
 ATTGAAAAACGAAAATCGTGTGTTGAAAAGAAGAATGCAACTTGTATATTGTATTAC  
 CTCTTTTTCAAGTGAATTAAATAGTTAATCATTTAACCAAGAAGATGTGTAGTGCCTTA  
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTAACCTCT  
 CCCAGTGAACTTATGGAACATTAAATTAGTACAATTAAAGTATATTAAAAATTGTAAAA  
 CTACTACTTTGTTAGTTAGAACAAAGCTCAAAACTACTTAGTTAACTGGTCATCTGAT  
 TTTATATTGCCTTATCCAAAGATGGGAAAGTAAGTCCTGACCAGGTGTTCCCACATATGCC  
 TGTTACAGATAACTACATTAGGAATTCTTAGCTTCTCATCTTGTGTGGATGTGTAT  
 ACTTTACGCATCTTCTTTGAGTAGAGAAAATTATGTGTGTCTGTGGCTTGTGAAAATG  
 GAACACCATTCTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTCTCCTCCT  
 GCATATTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAGTA  
 TCTCTAAATACAGGATTATAATTCTGCTTGAGTATGGTGTAACTACCTGTATTAGAAA  
 GATTTCAGATTCCATCTCCTTAGTTCTTTAAGGTGACCCATCTGTGATAAAAATA  
 TAGCTTAGTGCTAAATCAGTGTAACTTACATGGCTAAATGTTCTACAAATTAGAGT  
 TTGTCACTTATTCCATTGACCTAACAGAGAAAAATAGGCTCAGTAGAAAGGACTCCCTGG  
 CCAGGGCGCAGTGACTTACGCCGTAAATCTCAGCACCTTGGGAGGCCAAGGCAGGCAC  
 GAGGTAGGAGTTGGAGACCATCCTGCCAACATGGTGAACACCCGTCTACTAAAAATAT  
 AAAAATTAGCTGGGTGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC  
 GAGAATCACTTGAACTCAGGAGATGGAGGTTCACTGAGGCCGAGATCACGCCACTGCACTCC  
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAA

## **FIGURE 74**

MAARWRFWCVSVTMVALIVCDVPSASAQRKKEMVLSEKVSQMLEWTNKRPVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG  
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFAALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGPYSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

## FIGURE 75

AAGCAACCAAATGCAAGCTTGGGAGTTGTTCGCTGCCCTGCCGCTGCTCTGCTAGGGAGA  
 GAACGCCAGAGGGAGGGCGCTGGCCCGGCAGGCTCTCAGAACCGTACCGGCG**ATG**CTA  
 CTGCTGTGGGTGTCGGTGGTCGCAGCCTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA  
 GCAGAGGCAGGAGAGCAGCCAAAGCGCCAATGTGGTGCTGGTCGTGAGCGACTCCTCGATG  
 GAAGGTTAACATTCATCCAGGAAGTCAGGTAGTGAACACTTCCTTTATCAACTTTATGAAG  
 ACACGTGGACTTCCTTCTGAATGCCACACAAACTCTCAACATTGTTGCCATCACGCGC  
 AGCAATGTGGAGTGGCCTTCACTCACTAACAGAACATCTGGAAATAATTAAAGGGTAG  
 ATCCAAATTATAACACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATT  
 GGGAAACTGGACTATACTCAGGACATCACTCCATTAGTAATCGTGTGGAGCGTGACAAG  
 AGATGTTGCTTCTTACTCAGACAAGAAGGCAGGCCATGGTTAATCTTATCCGTAAACAGGA  
 CTAAAGTCAGAGTGTGGAAAGGGATTGGCAGAACATACAGAACAGCAGTAAACTGGTTAAGA  
 AAGGAAGCAATTAAATTACACTGAACCATTTGTTATTACTGGGATTAAATTACACACACCC  
 TTACCCCTCACCATCTGGAGAAAATTGGATCTTCAACATTCACACATCTCTTATT  
 GGCTGAAAAGTGTCTCATGATGCCATCAAAATCCAAAGTGGCACCTTGTCAAGAAATG  
 CACCTGTAGATTATTACTCTTCTTACAAAAAAACTGCACTGGAAAGATTACAAAAAAAGA  
 AATTAAAGAATATTAGAGCATTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGT  
 AAATTATTTGGCCCTTCATCAATTAGATCTTCTCAGAAAATATTGTCAATACCTCA  
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTATAAAATGAGCATGTACGAGGCTAG  
 TGCACATGTCGCTTTGATGATGGGACCAGGAATTAAAGCGGCCTACAAGTATCAAATG  
 TGGTTCTCTGTGGATATTACCTACCATGCTGATATTGCTGGAAATTCTCTGCCCTCAG  
 AACCTGAGTGGATACTCTTGTGCTTATCATCAGAAACATTAAAGAACATAAAGT  
 CAAAAACCTGCATCCACCCCTGGATTCTGAGTGAATTCCATGGATGTAATGTGAATGCCCTCA  
 CCTACATGCTCGAACTAACCACTGGAAATATATAGCCTATTGGATGGTCATCAATATTG  
 CCTCAACTCTTGATCTTCCTCGGATCCAGATGAATTAAACAAATGTTGCTGTAAAATTCC  
 AGAAAATTACTTATTCTTGGATCAGAAGCTTCATTATAAAACTACCCTAAAGTTCTG  
 CTTCTGTCCACCAGTATAATAAAGAGCAGTTATCAAGTGGAAACAAAGTATAGGACAGAAT  
 TATTCAAACGTTATAGCAAATCTTAGGTGGCACCAAGACTGGCAGAAGGAACCAAGGAAGTA  
 TGAAAATGCAATTGATCAGTGGCTAAAACCCATATGAATCCAAGAGCAGTT**TGA**ACAAAAAA  
 GTTAAAAATAGTGTCTAGAGATACTAAATATATTACAGATCATAATTATGTATT  
 AAATGAAACAGTTTAATAATTACCAAGTTGGCCGGCACAGTGGCTCACACCTGTAATC  
 CCAGGACTTTGGGAGGCTGAGGAAGCAGATCACAAGGTCAAGAGATTGAGACCACCTGGC  
 CAACATGGTGAACCCCTGTCTACTAAAATACAAAATTAGCTGGCGCGGTGGTCACA  
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGGAGGATCGCTTGAACCCGGAGGCAGCAG  
 TTGCAGTGAAGCTGAGATTGCCACTGTACTCCAGCCTGGCAACAGAGTGAAGACTGTGTCG  
 AAAAATAAAAATAAAATAATTACCAATTTCATTATTGTAAAGAATGTAGTG  
 TATTTAAGATAAAATGCCAATGATTATAAAATCACATATTTCAAAATGGTTATTATT  
 GGCCTTGTACAATTCTAACATTAGTGGAGTATCAAAGGATTGAAGCAAATACTGTA  
 ACAGTTATGTTCTTAAATAATAGAGAATATAAAATTGTAAATATGTATCATAAAAT  
 AGTGTATGTGAGCATTGATGGTGAaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  
 Aaa

## FIGURE 76

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDSFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPsRAAMWGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHSISNRVEAWTRDVAFLLRQEGRPMVNLI RNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFV IYLG LNLPH PYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPV DYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSNVVSLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDELTNAVFKPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMN PRAV
```

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

## FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**  
 GCCTCTCTGGCCTCCAACTTGTGGCTACATCCTAGGCCTCTGGGCTTTGGGCACACT  
 GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG  
 CAGTTGGCTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG  
 TGTGACATCTATAGCACCCCTCTGGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT  
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTTGGCATGAGATGCA  
 CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCCTTTC  
 ATCCTTGGAGGCCTCTGGGATTCAATTCTGTTGCCTGGAATCTCATGGGATCCTACGGGA  
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTGAGATTGGAGAGGCTTTACTTGG  
 GCATTATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTGCTCATCC  
 CAGAGAAATCGCTCCAACACTACGATGCCTACCAAGCCAACCTTGCACAGGAGCTC  
 TCCAAGGCCTGGTCAACCTCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT  
 ATGTG**TGA**AGAACCAAGGGCCAGAGCTGGGGGTGGCTGGTCTGTGAAAAACAGTGGACAG  
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTAGAAGGTGCTGCTGAGG  
 ATAGACTGACTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATG  
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTCTGTTTCCTCACCTGCTGCTC  
 CCCTGCCCTAAGTCCCCAACCCCTCAACTGAAACCCATTCCCTTAAGCCAGGACTCAGAGG  
 ATCCCTTGCCTCTGGTTACCTGGACTCCATCCCCAAACCCACTAATCACATCCACTG  
 ACTGACCCCTCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTCTAGCTATTGCTGG  
 GGATGGGAAGGAGAAGCAGTGGCTTGTGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
 TCCAAAGAAACTGATTGCCCTGGAACCTCCATCCACTCTGTTATGACTCCACAGTGTCC  
 AGACTAATTGTGCATGAACTGAAATAAAACCCTACGGTATCCAGGAAACAGAAAGCAG  
 GATGCAGGATGGGAGGGACAGGAAGGCAGCCTGGACATTAAAAAAATA

## **FIGURE 78**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIIPVAWNLHGILRDFYSPLVPSMKFEIGEALYLGISSLFSLIAGIILCFSCS
SQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

**FIGURE 79**

GCAC TGCT GCT GTCCC ATCAG CTGCT CTGAAG CTC **ATG** GTGCC CAGA ATCT CGCT CCTGC  
TTAT GTGT CAGT CTGT CTCC CTCT GTGT CCAAGG GAAGT CATCGCTCCGCTGGCTCAG  
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTGGAGCAG  
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC  
CTTCTGGCCCTGCTTGAGCTCTGCTGTCTTGATTCCCTTGGCCTCACAAACGATTGTTG  
TGAAGCTGAAGGTTCAGGGTGTGAATTCCCAGTGCCACTCATCTCCATCTCCAGTAAATGT  
GAAAGCAGAAGACGTTTCCCT**TGA**GAAGACATAGAAAGAAAATCAACTTCACTAAGGCATC  
TCAGAAACATAGGCTAAGGTATATGTGTACCACTAGAGAAGCCTGAGGAATTACAAAATG  
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
AGATTATCAGGAAATAAAAGTGGTTTCCAATGTACACACCTGTAAAA

## **FIGURE 80**

MVPRIFAPAYVSVC~~LLL~~CPREVIAPAGSEPWLQPA~~P~~RCGDKIYNPLEQCCYND~~A~~IVSLSE  
TRQCGPPCTFWPCFELCCLDSFGLTND~~F~~VVKLVQGVNSQCHSSPISSKCESRRRFP

**Signal peptide:**

amino acids 1-25

**FIGURE 81**

CTCCACTGCAACCACCCAGAGCC**ATG**GCTCCCGAGGCTGCATCGTAGCTGTCTTGCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTCTACGACCCCCTGCAGCACTGTT  
GCTATGATGATGCCCGTGTGCCCTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA  
GTCTGCTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA  
CTCAGCCGGACCTCGGATGACAGGCTTGTGCAGTGTCA**TAA**TGGAACATCAGGGAA  
CGATGACTCCTGGATTCTCCTCCTGGTGGCTGGAGAAAGAGGCTGGTGTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTGGGGCCAGAGAACACACACTCAACTGCCACTTCATT  
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGCCAGGGACTCTGAACCCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCAACCCCAAGGCTGGCTGGGAACCCTTCACCC  
TCTGTGAGATTTCCATCATCTCAAGTTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTATGTACTTATAATGAAAA

## **FIGURE 82**

MAPRGCIVAVFAIFCISRLLCSHGAPVAPMTPYLMCQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

**Signal peptide:**

amino acids 1-24

## FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCGCAGCGCTCACTCGCTCGCACTCAG  
 TCGCGGGAGGGTTCCCCGCGCCGGCCGTCCCGCCCTCCCCGGCACCAAGAAGTTCTCT  
 GCGCGTCCGACGGCGAC**ATG**GGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGA  
 TCCCTGCTCTCGCTCTTCCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTCAAGGTCGC  
 CACGCCGTATTCCCTGTATGTCTGTCCCAGGGGAGAACGTACCCCTCACCTGCAGGCTCT  
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTCTACAAGACGTGGTACCGCAGCTCGAGG  
 GGCAGGGTGCAGACCTGCTCAGAGGCCGGCCATCCGAAACCTCACGTTCCAGGACCTCA  
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTAGCGCCACGGGC  
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGAACCTGACCCCTGCTG  
 GATAGCGGCCTACTGCTGCCTGGTGGAGATCAGGCACCACACTGGAGCACAGGGT  
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACACTGTGTGGTGT  
 ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGTACGGGTGCCTGC  
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
 CTCCAACGCCGTGCCAGGAGCTGGTGCAGGACAGCAACATTCAAGGGATTGAAAACC  
 CCGGCTTGAAGCCTCACCACTGCCAGGGATAACCGAGGCCAAAGTCAGGCACCCCTG  
 TCCTATGTGGCCAGCGGCAGCCTCTGAGTCTGGCGGCATCTGCTTCGGAGCCAGCAC  
 CCCCCTGTCTCCTCCAGGCCCGAGACGTCTTCCATCCCTGGACCCCTGTCCCTGACT  
 CTCCAAACTTGAGGTCATC**TAG**CCCAGCTGGGGACAGTGGCTGTTGGCTGGGTCTGG  
 GGCAGGTGCATTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTGGCCTGGCCCTGGTTC  
 CCTCCCTCCTGCTCTGGCTCAGATACTGTGACATCCCAGAACGCCAGCCCTAACCCCTC  
 TGGATGCTACATGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTGGGTGCTGAG  
 ATTCTCCCCTAGAGACCTGAAATTCAACCAGCTACAGATGCCAAATGACTTACATTTAAGAA  
 GTCTCAGAACGTCCAGCCCTCAGCAGCTCTCGTTCTGAGACATGAGCCTGGGATGTGGCA  
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCCTCCAGGCACCAGACACAGGGCACGGTG  
 GAGAGACTCTCCCCGTGGCGCCTGGCTCCCCGTTGGCCAGGCTGCTCTGTGTC  
 AGACTTCCCTTTGTACACAGTGGCTCTGGGCCAGGCCTGCCACTGGCCATGCC  
 ACCTTCCCCAGCTGCCCTACCAAGCAGTTCTGAAGATCTGTCAACAGGTTAAGTCAAT  
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTGGTGGTCCGAAACGGGAAGTAC  
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTGGCAATCTGAGGCCAGGACAG  
 ATGTTGCCCAACCACTGGAGATGGTGTGAGGGAGGTGGTGGGCCCTCTGGGAAGGTGA  
 GTGGAGAGGGCACCTGCCCTCCCCATCCCCTACTCCCACTGCTCAGCGCGGGCC  
 ATTGCAAGGGTGCCACACAATGTCTGTCCACCCCTGGGACACTTCTGAGTATGAAGCGGGAT  
 GCTATTAAAAACTACATGGGAAAAAAAAAAAAAAAAAAAAAAAAGA

## **FIGURE 84**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLEASD
HHGNFSITMRNLTLDSGLYCCLVVEIRHHSEHRVHGAMELQVQTGKDAPSNCVVPSSSQ
DSENITAAALATGACIVGILCLPLLLLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPVDVFFPSLDPVPDSPNFEVI
```

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216

## FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTCGTCTCCATCTCTCCCTCCT  
 TTCCCCGCGTTCTCTTCCACCTTCTCTTCTCCACCTAGACCTCCCTGCCCTCC  
 TTTCTGCCACCGCTGCTCCTGGCCTCTCCGACCCGCTCTAGCAGCAGACCTCCTGG  
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCCTTCGTCTCCCTCCGA  
 CTCCGCTCCGGACCAGCGGCCTGACCCCTGGGAAAGG**ATG**GTTCCCGAGGTGAGGGTCCTC  
 TCCTCCTTGCTGGACTCGCGCTGCTGGTTCCCCCTGGACTCCCACGCTCGAGCCGCC  
 AGACATGTTCTGCCTTCCATGGAAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT  
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGGCCATGTGAGT  
 TGTACCGCCTCCACTGTCCGCTGTCCACTGCCCGAGCCTGTGACGGAGCCACAGCAATG  
 CTGTCCTAACGTGTGGAACCTCACACTCCCTCTGGACTCCGGGGCCACCAAAGTCTGCC  
 AGCACACAACGGGACCATGTACCAACACGGAGAGATCTCAGTGCCATGAGCTGTTCCCTCC  
 CGCCTGCCAACCAACCAGTGTGCCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCC  
 AACCTGCCCGAACCAAGGCTGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAACGCT  
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGTG  
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGAGAAAGAGAGGGCCGGCACCCAGC  
 CCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTGCCACTCAGACCCAAGGGAGCAG  
 GCAGCACACAATGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG  
 AAGACGTACTCCCACGGGAGGTGTGGCACCCGGCTTCCGTGCCTCGGCCCCCTGCC  
 CATCCTATGCACCTGTGAGGATGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT  
 ACCCCTGCCGTACCCCGAGAAAGTGGCTGGAAAGTGCTGCAAGATTGCCAGAGGACAAA  
 GCAGACCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCGGGTCT  
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACTGCCTCGCTTGCCTGGAACACGAGG  
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAG  
 AGAGGTGAAGTACCTGGCCAAGGCCACACAGCCAGAACTTCCACTGACTCAGATCAAGA  
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTCCGACTGCTCGCTGGCCCCAC  
 GAAGGTCACTGGAACGTCTCCTAGCCCAGACCCCTGGAGCTGAAGGTACGGCCAGTCCAGA  
 CAAAGTGACCAAGACATAACAAAGAC**TAAC**AGTTGCAGATATGAGCTGTATAATTGTT  
 ATTATATATTAATAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAA

## **FIGURE 86**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVVRHPQDPCSSDAGRKRGPGTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLV
KDEETEAQRGEVPGPRPHSQNLPLSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPG
AEGHGQSRQSDQDITKT
```

**Signal peptide:**

amino acids 1-25

## **FIGURE 87**

## **FIGURE 88**

MDSLRKMLISVAMLGAGAGVGYALLVITPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA  
TLQEAATTQENVAVWRKNWMVGGEGGASGRSP

**Signal peptide:**

amino acids 1-18

## FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCCGCTCCAAAGCTAACCTCGGGCTTGAGGGGAAGA  
 GGCTGACTGTACGTTCTTCTACTCTGGCACCCTCTCAGGCTGCC **ATG**GGGCCAGCACC  
 CCTCTCCTCATCTTGTGTCATGGTCGGGACCCCTCCAAGGACAGCAGCACCACCT  
 TGTGGAGTACATGGAACGCCACTAGCTGCTTAGAGGAACGGCTGCCAGTGCCAGGACC  
 AGAGTAGTCGGCATGCTGCTGAGCTGCCACTCAAGAACAAAGATGCTGCCACTGCTGGAG  
 GTGGCAGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCACCCATCTCGGGAGAGTGGA  
 TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTGCCCTGTGAGTAC  
 TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAAGAAGGATGAGAAGTAC  
 GATATGGTACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCG  
 ATTTGGTGGCCCAGCTGGCTATGGACCAAGGATCCACTGGGCAAACAGAGAAGATCTACG  
 TGTTAGATGGGACACAGAACACAGCCTTGTCTTCCAAGGCTGCGTACTTCACCCTT  
 GCCATGGCTGCCCGGAAAGCTCCCGAGTCCGGGTGCCCTCCCTGGTAGGCACAGGGCA  
 GCTGGTATATGGTGGCTTCTTATTTGCTGGAGGCCCTGGAAAGACACTGGTGGAGGTG  
 GTGAGATGGAGAACACTTGAGCTAATCAAATTCCACCTGGCAAACCGAACAGTGGTGGAC  
 AGCTCAGTATTCCCAGCAGAGGGCTGATCCCCCTACGGCTTGACAGCAGACACCTACAT  
 CGACCTGGTAGCTGATGAGGAAGGTCTTGGCTGTCTATGCCACCCGGAGGATGACAGGC  
 ACTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGACACACCA  
 TGTCCCAGAGAGAACATGCTGAGGCTGCCCTGTCTGTGGGACCCCTATGCGTCTATAA  
 CACCCGTCCTGCCAGTCGGGCCGCATCCAGTGCTCCTTGATGCCAGCGCACCTGACCC  
 CTGAACGGCAGCACTCCCTTATTTCCCCGAGATATGGTGGCCATGCCAGCCTCCGCTAT  
 AACCCCCGAGAACGCCAGCTCTATGCCGGATGATGGCTACCAGATTGTCTATAAGCTGGA  
 GATGAGGAAGAAAGAGGGAGGAGGTT **TGA**GGAGCTAGCCTGTTTGATCTTCTCACTC  
 CCATACATTATATTATCCCCACTAAATTCTTGTCTCATCTTCAAATGTGGCCAG  
 TTGTGGCTCAAATCCTCTATATTTAGCCAATGGCAATCAAATTCTTCAGCTCCTTGT  
 TCATACGGAACTCCAGATCCTGAGTAATCCTTAGAGGCCGAAGAGTCACCCCTCAATG  
 TTCCCTCCTGCTCCTGCCCATGTCACAAATTCAAGGCTAACGGATGCCAGACCCAGG  
 GCTCTAACCTTGTATGCCGGCAGGCCAGGGAGCAGGCAGCAGTGTCTTCCCTCAGAGTG  
 ACTTGGGGAGGGAGAAATAGGAGGAGACGTCCAGCTGTCCTCTCCTCACTCCTCCCT  
 TCAGTGTCTGAGGAACAGGACTTCTCCACATTGTTGTATTGCAACATTGCAATTAAA  
 AGGAAAATCCACAAA  
 AAAAAAAAAAAAAAAA

## **FIGURE 90**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLSGPLQGQQHHLVEYMERLAALERLAQCQDQSSRHAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVRVPFWGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDEQ
QWDTPCPRENAEAAFVICGTLVYVYNTPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV
```

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

## FIGURE 91

GACAGCTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCCGCTCACGCAG  
AGCCTCTCCGGCTTCCGCACCTTGAGCATTAGGCCAGTCTCCTCTCTCTAATCCAT  
CCGTCACCTCTCCTGTCATCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**  
CTCTCATGCTCAGTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTT  
GGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGAGGACGCAGCATCTCCTGTTCCGTC  
TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGGTTCTCAGGGCAGTTCTCTAGCGTGG  
TCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATCAAGGCAGG  
ACAAAACGGTGAAGGATTCTATTGGGAGGGCGCATCTCTGAGGCTGGAAAACATTAC  
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTCCCAGTCTACTACCAGAACGGCA  
TCTGGAGCTACAGGTGTCAGCACTGGGCTCAGTCCCTCATTCATCACGGATATGTT  
GATAGAGACATCCAGCTACTCTGTCAGTCCTCGGGCTGGTCCCCGGCCCACAGCGAAGTG  
GAAAGGTCCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC  
TGTGTTGATGTGGAGATCTCTGACCGTCCAAGAGAACGCCGGAGCATACTCTGCTGTGGCCTATT  
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACTTTTCA  
GCCTATATCGTGGCACCTGGTACCAAAGTACTGGAAATACTCTGCTGTGGCCTATT  
GCATTGTTGGACTGAAGATTCTTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACGGAC  
TGGAGAAGAACGACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGAC  
TCTGGATCCAGAGACGGCTACCCGAAGCTCTGCGTTCTGATCTGAAAATGTAACCCATA  
GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCT  
TCTCAGAGTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAGGTG  
GCGCGTGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTGTCTCCG  
ATCATGGGTACTGGTCCTCAGACTGAATGGAGAACATTGTATTCACATTAAATCCCCGT  
TTTATCAGCGTCTTCCCCAGGACCCCACCTACAAAAATAGGGTCTCCTGGACTATGAGTG  
TGGGACCATCTCCTCTCAACATAAATGACCAGTCCATTACCTGACATGTCGGT  
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCC  
ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAACAGGCCCTTGGCAAAGGGCCTCTGC  
AATCCCAGAGACAAGAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTCCCTCCAGGG  
GTGAAATG**TAG**GATGAATCACATCCCACATTCTTCTTAGGGATATTAGGTCTCTCCCA  
GATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTCCAGATGAAGGGGACTGCCGTG  
ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGAGGGAAAGAAGGCTGACATTACATT  
AGTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG  
TCAGGAATTCCCATCTCACAGGCTGTGGTAGATTAGTAGACAAGGAATGTGAATAATGC  
TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTGTTCATTATATTACACTTCAGTA  
AAAAAA

卷之三

## FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSS  
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQK  
AIWELQVSALGSVPPLISITGYVDRDIQLLCQSSGWFPRPTAKWKGPGQQLSTDRTNRDMH  
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKVT  
HRKAPQEVPHSEKRFRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTL  
PDHGYWVRLNGEHLYFTLNPRFISVFPPRTPKIGVFLDYECGTISFFNINDQSLIYTLTC  
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPESTNSSESSSQATTPLP  
RGEM

Signal peptide:

amino acids 1-17

### Transmembrane domain:

amino acids 239-255

## FIGURE 93

GCGATGGTGCGCCGGTGGCGGGCGGGTTGCGGAGGCTTCCTGGTCGGATTGCA  
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGC  
**CATG**AGGAGCCTGCCGAGCCTGGCGGCCTGCCCTGTGTGCTGCGCCGCCGCCGCC  
 CCGTCGCCTCAGCCGCCTCGGCGGGGAAATGTCACCGGTGGCGGGGGCCGCCGGGGCAGGTG  
 GACCGCTGCCGGGCCCCGGGTTGCGGGCGAGCCCAGCCACCCCTCCCTAGGGCAGCGC  
 TCCCACGCCAGGCCAGGGCCCCGAGGACCGGGCCCCCGCGGCCACCGTCCACCGACCCCTGGCTG  
 CGACTTCTCCAGGCCAGTCCCCGGAGACCACCCCTTTGGCGACTGCTGGACCCCTTCC  
 ACCACCTTCAGGCGCCGCTGGCCCTCGCCGACCACCCCTCCGGCGGCGAACGCACTTC  
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCCTTCGACGACCACGGCCCG  
 CGCCGACCACCCCTGTAGCGACCACCGTACCGCGCCACGACTCCCCGGACCCGACCCCG  
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCCCTC  
 TTGCGCTCCTCCAGAGTATGTAACTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT  
 GCAACCAGACCACAGGGCAGTGTGAGTGTGGCCAGGTATCAGGGCTTCACTGTGAAACC  
 TGCAAAGAGGGCTTTACCTAAATTACACTTCTGGCTCTGTCAGCCATGTGACTGTAGTCC  
 ACATGGAGCTCTCAGCATAACCGTGAACAGG**TAA**GCAACAGAGGGTGGAACTGAAGTTATT  
 TTATTTAGCAAGGAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTAACAAAG  
 GAGGATGAGGGTCAAGATTACAAAATATTTATATACTTTATTCTCTACTTTATATGT  
 TATATTTAATGTCAGGATTTAAAACATCTAATTTACTGATTTAGTTCTTCAAAAGCACTAG  
 AGTCGCCAATTTCTCTGGATAATTCTGTAAATTCATGGGAAAAAAATTATTGAAGAAT  
 AAACTGCTTCTGGAGGGCTTCAGGCATGAAACCTGCTAGGAGGTTAGAAATGTTCTT  
 ATGTTATTAAATATACATTGGAGTTGAGGAAATTGTTGTTGGTTATTCTCTCTA  
 ATCAAATTCTACATTGTTCTTGACATCTAAAGCTTAACCTGGGGTACCTAATTAA  
 TTTAACTAGTGGTAAGTAGACTGGTTACTCTATTACAGTACATTGAGACCAAAAG  
 TAGATTAAGCAGGAATTATCTTAAACTATTATGTTATTGGAGGTAATTAAATCTAGTGG  
 ATAATGTAAGTGTATCTAACGATTTGCCCTGTACTGCACTGAAAGTAATTATTGACCT  
 TATGTGAGGCACTTGGCTTTGTGGACCCCAAGTCAAAAAAACTGAAGAGACAGTATTAAAT  
 AATGAAAAAAATAATGACAGGTTAACTCAGTGTAAACCTGGTATAACCCAAAGATCTGCTGC  
 CACTTACGAGCTGTGTTCTGGCAAGTAATTCTTCACTGAGCTTGTCTCTCAAG  
 GTTGTGTGAAGATTAATGAGTTGATATATAAAATGCCTAGCACATGTCACTCAATAAA  
 TTCTGGTTGTTAATTCAAAGGAATTATGGACTGAAATGAGAGAACATGTTAACAG  
 ACTTTAGCTCCTGACAAAGAAGTGTAACTTACAGTAAATATTAAATGCTTTA  
 TAAATGATATTAACTGTTATGGAATTATGTATCATATTGTAGTTATTAAAATGAGAAG  
 AGGCTGGCGCGGTGGCTACGCCGTAAATCCTAGCACATTGGGAGGCCAAGGCAGGGTGGAT  
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACACCCGTCTACTAAA  
 AATACAAACAAATTAGCTGGCGTGGCACACACCTGTAGTCCCAGCTACTGGGAGGCT  
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAAGATCGGCCACT  
 GCACCTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTAAAAAAAAAAAAAA

## **FIGURE 94**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGIALLCCAAAAAVASAASAGNVTGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPPTPPAAERTS
TTSQAPTRPAPTTLSSTTGPAPTPVATTVPAPTPRTPTPDLSSNSVLPTPPATEAPS
SPPPEYVCNCVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

**FIGURE 95**

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGCGGCCTGCTGCTGGCTGCTTTCTGGCTTGG  
TCTCGGTGCCAGGGCCCAGGCCGTGGTTGGGAAGACTGGACCCCTGAGCAGCTCTGGG  
CCCTGGTACGTGCTGCGGTGGCCTCCGGAAAAGGGCTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGTGGTGGTGGCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC  
AGCACGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTGAGAATCCCTCAATAGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTCACTCAGCTGGAGTTGGGACGAGCCCTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGGCCAGGAGGCCATGGGCTCTCACCAAGTGGAGCAGGAGC  
CTGGGCTTCCTGTACAG**TAG**CAGGCCAGCTGCAGAAGGACCTCACCTGTGCTCACAGAT  
CCTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGCCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCGGGCCAGCACCAGCTCAGAATAAAGCGATT  
CACAGCA

## **FIGURE 96**

MGGLLLAFLALVSVPRAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNLRTLSSQHGLGGCDQSVMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

amino acids 1-20

## FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGAC**ATG**CTGCTGCTGCTGCTGCC  
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT  
 CCGTGACGGTGCAGGAAGGCCTGTGTCCATGTGCCCTGCTCCTCTCCTACCCCTCGCAT  
 GGCTGGATTTACCTGGCCCAGTAGTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA  
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGAGGAGACTCGGGACC  
 GATTCCACCTCCTGGGGACCCACATACCAAGAATTGCACCCCTGAGCATTGAGAGATGCCAGA  
 AGAAGTGTGCGGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
 ACATCACCGGCTCTGTGAATGTGACAGCCTGACCCACAGGCCAACATCCTCATCCCAG  
 GCACCCCTGGAGTCCGGCTGCCCTCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG  
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCACCAC  
 CCGCTCCTCGGTGCTCACCTCATCCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
 AGGTGACCTTCCCTGGGCCAGCGTGACCACGAACAAGACCGTCCATCTAACGTGTCCTAC  
 CCGCCTCAGAACTTGACCATGACTGTCTCCAAGGAGACGGCACAGTATCCACAGTCTGGG  
 AAATGGCTCATCTGTCACTCCCAGAGGGCCAGTCTGCGCCTGGTCTGTGCAGTTGATG  
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCCTGTGCCCT  
 TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCTGGGTGCACCTGAGGGATGCAGCTGA  
 ATTTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGAGCTGGAGGCCACAGCCCTG  
 GTCTTCCCTGTCCTCTCGTCATCTCGTTGAGGTCTGCAGGAAGAAATCGGCAAG  
 GCCAGCAGCGGGCGTGGAGATAAGGGCATAGAGGATGCAAACGCTGTCAGGGGTTCAGCCT  
 CTCAGGGGCCCTGACTGAACCTGGGCAGAACAGACAGTCCCCAGACCAGCCTCCCCAGCT  
 TCTGCCCGCTCCTCAGTGGGGAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
 GAAGCCTTGGGACTCGCGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
 ACAGA**TGA**GAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA  
 GAAGTCAGAGGCTGATTCTGTAGAATTAAACAGCCCTAACGTGATGAGCTATGATAACACT  
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTAGAGTCAAAGTATCTAAACCTGAAT  
 CCACACTGTGCCCTCCCTTTATTTTTAACTAAAAGACAGACAAATTCTTA

## **FIGURE 98**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPSCFSYPSHGWIYPGPVHGYWF  
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLISRSDAGRYFRRMEKG  
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVS  
PLDPSTTRSSVLTЛИPQPQDHGTSЛTCQVTFPGASVTTNKTВHLNVSYPPQNLTMVFQGDG  
TVSTVLGNSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
HLRDAAEFTCRAQNPLGSQQVYLNVLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS  
CRKKSARPAAGVGDTGIEDANAVGSASQGPLTEPWAEDSPPDQPPPASARSSVGEGELOYA  
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

**FIGURE 99**

GACGCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAAGACCTGTTCTG  
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTCACCCCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTCCGGAGGACAGGAGGCCAGGA  
AGGTGTCCCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGAAGGCCACGTTCACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT  
ACATCTTTACTGCAAAGACCAGCACCATGGGGCCTGCTCCACATGGAAAGCTTGTGGGT  
AGGAATTCTGATACCAACCAGGGAGGCCCTGGAAGAATTAAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTCACGCCCTGCAGACGGGAAGCTGCCTCCGAACACTAGG  
CAGCCCCGGGTCTGCACCTCCAGAGCCCACCCCTACCACCAAGACACAGAGCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCTTCCCTGCTCCCACCCACCTGACTCCAAATAAGTCCT  
TTTCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGK
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

**Important features:**

**Signal peptide:**

amino acids 1-17

## FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCAGGGACTGGAAGTCATCGGGCAGAGGTCTCAC  
AGCAGCCAAGGAACCTGGGGCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA  
TCCTGCTTGCCTGGCAACAGGGCTTGTAGGGGAGAGACCAGGATCATCAAGGGGTTGAG  
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTCGAGAAGACGCGGCTACTCTGTGG  
GGCGACGCTCATGCCCGAGATGGCTCCTGACAGCAGCCCAGTGCCTCAAGCCCCGCTACA  
TAGTTCACCTGGGGCAGCACAAACCTCCAGAAGGAGGGCTGTGAGCAGACCCGGACAGCC  
ACTGAGTCCTTCCCCACCCCGCTTCAACAACAGCCTCCCCAACAAAGACCCACCGCAATGA  
CATCATGCTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGCTGTGCAGCCCTCACCC  
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTCGGCTGGGAGCAGCAGTCC  
AGCCCCCAGTTACGCCTGCCTCACACCTTGCATGCGCCAACATCACCATTGAGCACCA  
GAAGTGTGAGAACGCCTACCCGGAACATCACAGACACCAGGTGTGCCAGCGTGCAGG  
AAGGGGGCAAGGACTCCTGCCAGGGTGAUTCCGGGGCCCTCTGGTCTGTAACCAGTCTTT  
CAAGGCATTATCTCCTGGGCCAGGATCCGTGCGATCACCGAAAGCCTGGTGTACAC  
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAATGACTGGACCCA  
CCCACACAGCCCATCACCCCTCATTCCACTGGTGTGGTCTGTTCACTCTGTTAAT  
AAGAAACCTAACGCAAGACCCCTACGAACATTCTGGCCTCTGGACTACAGGAGATG  
CTGTCACTTAATAATCAACCTGGGTTGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT  
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTGTTCTGTTGATCCCCAGCCCCA  
AAGACAGCTCCTGGCCATATATCAAGGTTCAATAAATATTGCTAAATGAAAAA  
AAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 102**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIA
PRWLTAAC
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLV
KMASPVSITW
AVRPLTLSSRCVTAGTSC
LISGWGSTSSPQLRLPHTLRCANITIIEHQKCENAYPGNITDTM
VCASVQEGGKDSCQGDSGGPLVCNQSLQGIISWGQDPCA
ITRKPGVYTKVCKYVDWIQETMKNN
```

**Important features:**

**Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

## **FIGURE 103**

GAGCAGTGTCTGCTGGAGCCG**ATG**CCAAAACCATGCATTCTTATTCAATTGTTT  
TCTTTATCTGTGGGCCTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA  
GTGAAAATAGAAGTTGCATCGTCAGAAAAGCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA  
CACAAAATGAAGGCCACCCAAATGGTTGTTCTGGTGGCAAGTCATAAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATAACCCCTTCATT  
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTG  
AGATTGAACTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGAAATTGA  
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTAGAAGATATTTAAGA  
AGAATGACCATGATGGTATGGCTTCATTCTCCAAGGAATACAATGTATACCAACACGAT  
GAACTA**TAG**CATATTGTATTCTACTTTTTTTAGCTATTACTGTACTTATGTATA  
AAACAAAGTCACTTCTCCAAGTTGTATTGCTATTTCCCCTATGAGAAGATATTTGA  
TCTCCCCAATACATTGATTTGGTATAATAATGTGAGGCTGTTGCAAACTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 104**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDFISPKEYNVYQHDEL
```

**Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214

**FIGURE 105**

CAGAA**ATG**CAGGGACCATTGCTTCTTCAGGCCTCTGCTTCTGCTGAGCCTCTTGGAGCT  
GTGACTCAGAAAACCAAAACTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCATAAA  
CACTCACTGCACCTGCAACCATGGATATACTCTGGATCTGGGAGAAACTATTCACATTCC  
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTG**TAA**TCCCAGTTCTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTCAAGGAGTTGAGACCAGCCTGGCCAACATAGTGAACAC  
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGCGTGGTGGTGCATGCCTGCAATCCAGT  
TACTCGGGAGGGCTGAGGCAGGAGAATCGCTTGAACTCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTAAAAAGAAAAGA  
TAGTTTCTTGTTCATTCGCGACTGCCCTCTCAGTGTTCCTGGATCCCTCCAAATAA  
AGTACTTATATTCTC

## **FIGURE 106**

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL  
ETCNARHGGSRL

**Signal peptide:**

amino acids 1-18

**FIGURE 107**

CAAGCAGGT CATCCCCTGGTGACCTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGCAC  
AGGGAAAGGGTGACCTCTGAGATTCCCCTTCCCCCAGACTTGGAAAGTGACCCACC**ATGG**  
GGCTCAGCATCTTTGCTCCTGTGTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
TTCAATGGCACTGAGTGTGGCGTAACTCACAGCCGTGGCAGGTGGGCTGTTGAGGGCAC  
CAGCCTGCCTGCGGGGTGTCTTATTGACCACAGGTGGGCTCACAGCGGCTCACTGCA  
GCGGCAGCAGGTACTGGGTGCCTGGGAAACACAGCCTCAGCCAGCTCGACTGGACCGAG  
CAGATCCGGCACAGCGGTTCTGTGACCCATCCCGCTACCTGGGAGCCTCGACGAGCCA  
CGAGCACGACCTCCGGCTGCTGCCTGCCTGCCGTCCCGTAACCAGCAGCGTTCAAC  
CCCTGCCCTGCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGG  
ATCACCAACCACCCACGGAACCCATTCCGGATCTGCTCCAGTGCCTAACCTCTCCATCGT  
CTCCCATGCCACCTGCCATGGTGTATCCGGAGAACATCACGAGCAACATGGTGTGCAG  
GCGCGTCCGGGCAGGATGCCTGCCAGGGTATTCTGGGGCCCTGGTGTGGGG  
GTCCTCAAGGTCTGGTGTCTGGGGTCTGTGGGCCCTGTGGACAAGATGGCATCCCTGG  
AGTCTACACCTATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACA**TGAC**  
CTGTTCTCCACCTCCACCCCCACCCCTTAACCTGGTACCCCTCTGCCCTCAGAGCACC  
AATATCTCCTCCATCACTCCCTAGCTCCACTCTGTTGGCCTGGAACCTCTTGGAACTT  
TAACTCCTGCCAGCCCTCTAAGACCCACGAGCGGGTGAGAGAAGTGTGCAATAGTCTGGA  
ATAAAATATAATGAAGGAGGGCAAAAAAAAAAAAAA

## **FIGURE 108**

MGLSIFLLLGVLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDGGPLVCGGVLQGLVSWGSVGPGQDGIPGVYTYICKYVDWIRMIMRNN

### Signal peptide:

amino acids 1-17

## FIGURE 109

GC GGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCGTCCCTCGC  
 CGCGTCCCGGAAGCCTGGAGCCGGCGGGAGCCCCCGCCTCGCC**ATG**TGGCGAGCTCAGCA  
 ACAGGTTCCAAGGAGGGAAAGGCAGTCTGGCTCAAAGCCCAGGAGAGGAGGCTGGCC  
 GAGATCAACCGGGAGTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCAGAAAA  
 GCTCACAGCCTCAAAGAGAAGTACATGGAGTTGACCTGAACAATGAAGGCAGATTGACC  
 TGATGTCTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
 AAGATGATCTCAGAGGTGACAGGGAGGGTCAGTGACACTATATCCTACCGAGACTTGTGAA  
 CATGATGCTGGGAAACGGTCGGCTGCCTCAAGTTAGTCATGATGTTGAAGGAAAAGCCA  
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCC**TGA**  
 GGACCCCGCCTGGACTCCCCAGCCTCCACCCATACCTCCCTCCGATCTGCTGCCCTT  
 CTTGACACACTGTGATCTCTCTCTCATTGTTGGTCAATTGAGGGTTGTTGTGTT  
 TCATCAATGTCTTGTAAAGCACAAATTATCTGCCTAAAGGGCTCTGGTCGGGAATCC  
 TGAGCCTTGGTCCCCCTCCCTCTCTTCCCTCCCTCCGCTCCGTGCAAGAGGCTG  
 ATATCAAACCAAAACTAGAGGGGGCAGGCCAGGGCAGGGCTTCCAGCCTGTGTTCCC  
 CTCACTGGAGGAACCAGCACTCTCCATCCTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC  
 ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTGGAGTAGGGACAAGG  
 CTGCAGGGCCTTTGGTTCCCTGGACAGTGCATGGTCCAGTGCTCTGGTGTACCC  
 AGGACACAGCCACTGGGCCCGCTCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT  
 CATCCTCAGTGATGTGAAGGTGGAAAGGAAAGGAGCTTGGCATTGGAGCCCTCAAGAAGG  
 TACCAAGGAACCTCCAGTCCTGCTCTGGCACACCTGTGCAGGCAGCTGAGAGGCAG  
 CGTGCAGCCCTACTGTCCTACTGGGGCAGCAGAGGGCTCGGAGGCAGAAAGTGAGGCCTG  
 GGGTTGGGGAAAGGTCAAGTCAGTGCTGTTCCACCTTGTAGGGAGGATACTGAGGGGAC  
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
 CTGAGAAATACAAGGTTGCTTGTCTGACCCAACTGCTGAAAAA

## **FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTA  
FKEKYMEFDLN  
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMM  
MLGKRSAVLKLVM  
MFEKGKANESSPKPVGPPP  
ERDIASLP

## FIGURE 111A

CGCGCTCCCCGCGCCCTCCTCGGGCTCCACGCGTCTTCCCCGAGAGGCAGGCCTCTCCA  
 GGAGCGGGGCCCTGCACACC**ATG**GCCCGGGTGGCAGGGTGGCGCCGCGCC  
 CGCCTGGCGCTGGCCTTGGCGCTGGCGAGCGTCTGAGTGGGCCTCCAGCGTCGCCTGCC  
 CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGCTGGCCTCCGCGGGTTC  
 CTCGGGGCATCCCCCGAACGCTGAGCGCTTGACCTGGACAGAAATAATATCACCAGGATC  
 ACCAAGATGGACTTCGCTGGCTCAAGAACCTCGAGTCTGCATCTGAAAGACAACCAGGT  
 CAGCGTCATCGAGAGAGGCGCTTCCAGGACCTGAAGCAGCTAGAGCAGTGCCTGAACA  
 AGAATAAGCTGCAAGTCCTCCAGAATTGCTTCCAGAGCAGCCGAAGCTCACCAAGACTA  
 GATTGAGTAAAACCAGATCCAGGGATCCCAGGAAGGCGTCCGCGGATCACCGATGT  
 GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTCCGAGCGC  
 TGCGGATTGGAGATCCTTACCCCAACAACAACATCAGTCGCATCCTGGTCAACCAGC  
 TTCAACCACATGCCGAAGATCCGAACTCTGCGCCTCCACTCCAACCACCTTACTGCGACTG  
 CCACCTGGCCTGGCTCTCGGATTGGCTCGCAGCGACGGACAGTTGCCAGTTCACACTCT  
 GCATGGCTCTGTGCATTGAGGGCTTCAACGTGGCGATGTGCAGAAGAAGGAGTACGTG  
 TGCCCAGCCCCCCTCGGAGCCCCCATCCTGCAATGCCACTCCATCTCCTGCCCTCGCC  
 CTGCACGTGCAGCAATAACATCGTGGACTGTCAGGAAAGGGCTTGATGGAGATTCTGCCA  
 ACTGCCGGAGGGCATCGTCAAACAGAACCTCCATCAAAGCCATCCCTGCA  
 GGAGCCTCACCCAGTACAAGAAACTGAAGCGAATAGACATCAGCAAGAACATCAGATATCGGA  
 TATTGCTCCAGATGCCTCCAGGGCTGAAATCACTCACATCGCTGGTCTGTATGGAAACA  
 AGATCACCGAGATTGCCAAGGGACTGTTGATGGGCTGGTCCCTACAGCTGCTCTCCTC  
 AATGCCAACAGATCAACTGCCTGCGGGTGAACACGTTCAAGGACCTGCAGAACCTCAACTT  
 GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGCTTCGCCCCCTGCAGT  
 CCATCCAGACACTCCACTTAGCCAAAACCCATTGTCAGCAGGACTGCCACTTGAAGTGGCTG  
 GCCGACTACCTCCAGGACAACCCATCGAGACAAGCGGGCCGCTGCAGCAGCCCGCG  
 ACTGCCAACAGCGCATGCCAGATCAAGAGCAAGAACGTTCCGCTGTCAGGCTCCGAGG  
 ATTACCGCAGCAGGTTCAGCAGCGAGTGCTCATGGACCTCGTGTGCCCCGAGAACAGTGTG  
 TGTGAGGGCACGATTGTGGACTGCTCAAACAGAACAGCTGGTCCGCATCCCAAGCCACCTCCC  
 TGAATATGTCAACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA  
 TCTCAAGAAGTTGCCAACCTGCGAAAATAATCTGAGTAACAATAAGATCAAGGAGGTG  
 CGAGAGGGAGCTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCT  
 GGAGACCGTGACGGCGTGTCCGTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA  
 GTAACCTGATCAGCTGTGAGTAATGACACCTTGCCGGCTGAGTCGGTGAGACTGCTG  
 TCCCTCTATGACAATCGGATACCACCATCACCCCTGGGGCTTCACCACGCTTGTCTCCCT  
 GTCCACCATAAACCTCTGTCACCCCTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA  
 AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGAACCCCTAGGTGCCAGAACGCATTTCTC  
 AAGGAGATTCCCACCCAGGATGTGGCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG  
 TAGCTGCCAGCTGAGCCCGCGTGCCCGAGCAGTCACCTGTATGGAGAACAGTGGTGC  
 GCAGCAACAAGGGCTCCGCGCCCTCCCCAGAGGCATGCCAAGGATGTGACCGAGCTGTAC  
 CTGGAAGGAAACCACCTAACAGCGTGCCTGCCAGAGAGACTGTCGCCACCTGACGCT  
 TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCACTAACATGTCTC  
 ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCACGCCCTCAAC  
 GGGCTCGGGTCCCTGCGAGTGCTAACCCCATGGCAATGACATTCCAGCGTTCTGAAGG  
 CTCCTCAACGACCTCACATCTTCCCATCTGGCGTGGGAACCAACCCACTCCACTGTG  
 ACTGCAGTCTCGGTGGCTGCGAGTGGTGAAGGCAGGGTACAAGGAGCCTGGCATGCC  
 CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTACCACCCCAACCCACCGCTT  
 CCAGTGCAAAGGGCAAGTGGACATCAACATTGTGGCAAATGCAATGCCCTGCCAGCC  
 CGTGCAAGAATAACGGGACATGCACCCAGGACCCCTGTGGAGCTGTACCGCTGTGCCCTGCC

## **FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA  
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTCAGCTGCTCCTGCCCTC  
 TGGGCTTGAGGGGAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA  
 AACAAATGCCACCTGCGTGGACGGGATCAACAACACTACGTGTGTATCTGTCCGCCTAACTACAC  
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCCTGAGCTGAACCTCTGTCAGCATG  
 AGGCCAAGTGCATCCCCCTGGACAAAGGATTCACTGCGAGGTGAGCTGCCCTGGCTACAGCGGG  
 AAGCTCTGTGAGACAGACAATGATGACTGTGAGGCCACAAGTGCCGCCACGGGCCAGTG  
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCTCAGGCTCAGTGGACCCCTCTGTG  
 AACACCCCCCACCACGGTCTACTGCAGACCAGCCATGCGACCAAGTACGAGTGCCAGAAC  
 GGGGCCAGTGCATCGTGGTCAGCAGGAGGCCACCTGCCCTGCCACCAGGCTTCGCCGG  
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTCGTGGCAAAGACTCCTACGTGGAACGG  
 CCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGCCACTGACAAGGACAAC  
 GGCATCCTTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCGAGGCCACGT  
 GCGGCTGGTCTATGACAGCCTGAGTCCCCCTCAACCACAGTGTACAGTGTGGAGACAGTGA  
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTACGCTAAACAGACCCCTGAACCTAGTAGT  
 GACAAAGGAACCTCAAAGAGCCTGGGAAGCTCCAGAACAGCAGCAGTGGGCATCAACAG  
 CCCCCTCTACCTGGAGGCATCCCCACCTCCACCGGCCCTCCGCCCTGCCAGGGCACGG  
 ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACAGAGCTG  
 GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTGCACCGT  
 GTGCAAGCACGGCCTGTGCCCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG  
 GCTGGACCGGCCACTCTGCAGACCAGGAGGCCACCTGCCCTGCCACAGATGCCAC  
 CATGGAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCAGGGCTATGGAGG  
 GGACTTGTGTGACAACAAGAAATGACTCTGCCAATGCCCTGCTCAGCCTCAAGTGTACCATG  
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCCTGTGCCAGCCGGCTTAGCGGC  
 GAGCACTGCCAACAAAGAGAATCCGTGCCCTGGACAAGTAGTCCGAGAGGTGATCCGCC  
 GAAAGGTTATGCATCATGTGCCACAGCCTCAAGGTGCCCATCATGGAATGTCGTGGGGCT  
 GTGGGCCCAAGTGTGCCAGGCCACCCGCAGCAAGCGGGAAATACGTCTTCAGTGCACG  
 GACGGCTCTCGTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCCTGCCCTCGCTGTT  
 CTAAAGGCCCTGCCCTGCCACCTCTGGACTCCAGCTTGTGATGGAGTTGGACAGCC  
 ATGTGGGACCCCTGGTATTGACATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA  
 AGAGAATATTAAGTATATTGTAAAATAACAAAAAATAGAACCTAAAAA  
 AAAAAA

## FIGURE 112

MAPGWAGVGA AVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN  
 AERLDLDRNNITRITKMDFAGLKNLRLVHLEDNQSVIERGAFQDLKQLERLRLNKNKLQVL  
 PELLFQSTPKLTRLDSNQIQQGIPRKAFRGIDVKNLQLDNNHISCIEDGAFRALRDLEIL  
 TLNNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL  
 RGFNVADVQKKEYVCPAPHSEPPSCNANSICSPSPCTCSNNIVDCRGKGLMEIPANLPEGIV  
 EIRLEQNSIKAI PAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK  
 GLFDGLVSLQLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTI SKGLFAPLQSIQTLHL  
 AQNPVCDCHLKWLADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS  
 SECFCMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDRLNDNEVSVLEATGIFKKLPN  
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGQNQLETVHGRVFRGLSGLKTLMLRSNLISCV  
 SNDTFAGLSSVRLLSLYDNRITTITPGAFTTLVSLSTINLLSNPNCNCNCHLAWLGKWLKR  
 IVSGNPRCQKPFILKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGLR  
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHTLIDLSNNISMLTNYTFSNMSHLSTLIL  
 SYNRLRCIPVHAFNGLRSLRVLTGHNDI SSVPEGSFNDLTSLSHLALGTNPLHCDCSRWL  
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFQCKGPVDINIVAKCNACLSSPCKNNGT  
 CTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEGQR  
 CEINPDDCEDNDCEENNATCVDGINNYVCICPPNYTGECLCDEVIDHCVPELNLQHEAKCIP  
 DKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMV  
 LLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP  
 QANISLQVATDKDNGILLYKGNDPLALELYQGHVRLVYDSLSSPTTVYSVETVNDGQFHS  
 VELVTLNQTINLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF  
 HGCIEHVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC  
 DQEARDPCILGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKNDSANACSAFKCHHGQCHISD  
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIIRRQKGYASCATASKVPI  
 MECRGCGPQCCQ  
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

**FIGURE 113**

GGATGCAGGACGCTCCCTGAGCTGCCTGTACCGACTAGGTGGAGCAGTGTTCCTCCGCA  
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTCAGTTCTGTCT  
CCGGCAGGCTTGAGGAATGAAGGCTGCAGGCATTCTGACCCCTCATTGGCTGCCTGGTCACAG  
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACGGCAAAATATTCTCGAGGGCTGGCCTG  
GACAATTACTGGGCCTTCAGCCTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA  
CAACACCACAGCCCCGACGGCCTGGATGACGGCAGCAGTCAGTATGGCATCTTCCAGATCA  
ACAGCTTCGCGTGGTGCAGACGCGAAAGCTGAAGGAGAACAAACCAACTGCCATGTCGCCTGC  
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA  
GACACAAGGAATGAACATTGGCAAGGCTGGAAGAACATTGTGAGGGCAGAGACCTGTCCG  
AGTGGAAAAAAGGCTGTGAGGTTCCTAAACTGGAACTGGACCCAGGATGCTTGAGCAAC  
GCCCTAGGATTGCAGTGAATGTCAAATGCCTGTGTATCTTGTCCCCTTCCTCCAAATA  
TTCCTTCTCAAACCTGGAGAGGGAAAATTAGCTATACTTTAAGAAAATAAATATTCCAT  
TTAAATGTC

## **FIGURE 114**

MKAAGILTLLIGCLVTGAESKIIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCCHVACSLITDDLTDAAIICARKIVKETQGMN  
YWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**

amino acids 1-19

## FIGURE 115

CAGGCCATTGCATCCCACTGTCCTGTGTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT  
 CATGTGTTAAAACGCCAAGCTGAATATATC**ATG**CCCCTATTAAAACCTGTACATGGCTCCC  
 CATTGGTTTGAGAAAAGTTCAAGCTTTACCTGGTGTGCCTGTATCCCAGTGTTC  
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGTCACTTCCCAGATCTGCTCTCAC  
 CAAGAGAGATTCTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA  
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTAAGGAA  
 ACATTCAAGTCCCTGTCTCACATAGACCTGATGTCCTCTATCCATCTAAATGTCACCAG  
 CTTGACTCAGTTGTCCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATCCTGC  
 TGCTCTCCATCAACAGATAACGAAAGGAAGAAAATCTGACTTGGCACTGGAAGCCCTAGTA  
 CAGCTGCGTGGAAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG  
 TTATGACGAGAGAGTCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC  
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCAGACAAACAGAAAATCTCC  
 CTCCCTCACAGCTGCACGTGTGCTTACACACCAAGCAATGAGCACTTGGCATTGTCCC  
 TCTGGAAGCCATGTACATGCAGTGCCCAGTCATTGCTGTTAATTGGGTGGACCCCTGGAGT  
 CCATTGACCACAGTGTACAGGGTTCTGTGAGCCTGACCCGGTGCACTTCTCAGAAGCA  
 ATAGAAAAGTTCATCCGTGAACCTCCTAAAAGCCACCATGGCCTGGCTGGAAGAGCCAG  
 AGTGAAGGAAAATTTCCCTGAAGCATTACAGAACAGCTTACCGATATGTTACCAAAC  
 TGCTGGTA**TAA**TCAGATTGTTTAAGATCTCCATTAATGTCATTTATGGATTGTAGACC  
 CAGTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTAAAAAATAAA  
 CTTGAGTCTTGAATGTGAGCCACTTCCCTATATACCACACCTCCCTGCCACTTTCAGAAA  
 AACCATGTCTTATGCTATAATCATTCAAATTGGCCAGTGTGTTAAGTTACAAATGTGGTG  
 TCATTCCATGTTCAAGCAGAGTATTTAATTATTTCTGGGATTATTGCTCTGTCTA  
 TAAATTGAAATGATACTGTCCTAATTGGTTTCTAGTTAAGTGTATCATTATCAA  
 AGTTGATTAATTGGCTTCAGTATAATGAGAGCAGGGCTATTGTTAGTCCAGATTCAAT  
 CCACCGAAGTGTTCAGTGTCACTGTCTGGAAATTGGCTGTCTTGCCTGGATC  
 CATAGCGAGAGTGCTCTGTATTTTTAAGATAATTGTATTTGCACACTGAGATATAA  
 TAAAAGGTGTTATCATAAAAAAAAAAAAAAA

## **FIGURE 116**

MPLLKLVHGSPLVGEFKLFTLVSACIPVFRILARRKKILFYCHFPDLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD  
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLLSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

## FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGCGGCAGAACCAATGTTGGACTTCGCGATCTT  
 CGCCGTTACCTTCTTGCCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTCCAGAC  
 AAGCTGCAGGAATTCCAGGGATTACTCCAACGTAAAGAAAAAGATGGTAATCTTCCAGATATT  
 GTGAATAGTGGAAAGTTGCATGAGTTCCTGGTTAATTGCATGAGAGATATGGGCCTGTGGT  
 CTCCTCTGGTTGGCAGGCCCTCGTGGTAGTTGGCACTGTTGATGTACTGAAGCAGC  
 ATATCAATCCAATAAGACATCGGACCCCTTGAAACCAGTGAAGTCATTATTAAGGTAT  
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAATTGTATGAAAATGGTGT  
 GACTGATTCTCTGAAGAGTAACTTGCCCTCCTAAAGCTTCAGAAGAATTATTAGATA  
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTGGTTTGCT  
 ATGAAGTCTGTTACACAGATGGTAATGGTAGTACATTGAAGATGATCAGGAAGTCATTG  
 CTTCCAGAAGAACATGGCACAGTTGGTCTGAGATTGGAAAAGGCTTCTAGATGGTCAC  
 TTGATAAAAACATGACTCGGAAAAAACATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTCATTGACTC  
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTCTG  
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGCAATCTGTTTTAACCACCTCTGAA  
 GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTGGAAATGGCCTGTTACTCC  
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTGTGAAACTGTTGAACTGCCA  
 AACTGACTCCAGTTCTGCCAGCTCAAGATATTGAAGGAAAATTGACCGATTATTATT  
 CCTAGAGAGACCCTCGTCCTTATGCCCTGGTGTGGTACTTCAGGATCCTAATACTGGCC  
 ATCTCCACACAAGTTGATCCAGATCGGTTGATGATGAATTAGTAATGAAAACCTTCT  
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTGCATATATGGTGA  
 CACA  
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTCTGGAGGGACAGGTTATTGA  
 AACAAAGTATGAACGGTAACATCATCAAGGGAAGAAGCTGGATCACTGTCTCAAAGAGAT  
 ATAAAATTAAATTGATTGAGGAAAACAACCATTAAAAAA  
 AAATCTATGTTGAATCCTTTATAAACCAAGTATCACTTGTAAATATAAACACCTATTGTAC  
 TTAA

## **FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
ERYGPVVSFWFGRRLVVSLGTVDVLKQHINPNKTSDFETMLKSSLRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQE VIRFQKNHGTWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSEEVQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIIPRETLVLYALGVVL  
QDPNTWPSPHKFDPDRFDELVMKTSSLGFSGTQECPELRFAYMVT TVLLSVLVKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

## FIGURE 119

CTAGATTGTCGGCTTGCAGGGAGACTTCAGGAGTCGCTGTCTGAACCTCCAGCCTCAGA  
GACCGCCGCCCTTGTCCCCGAGGGCC**ATG**GGCCGGTCTCAGGGCTTGTGCCCTCTCGCTTC  
CTGACGCTCCTGGCGCATCTGGTGGTCATCACCTATTCTGGTCCCAGGACAGAACAT  
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTAGCTGG  
TGGCCGCGCTCTGTCAACAGCACCCAGAGCCTCATCTCCATTGGGCTCACTGTAGTGCATCCGT  
GGCCCTGTCCCTTCTCATATTGAGCGTTGGGAGTGCACGTACGTATTGGTACATTTGTCT  
TCTGCAGTGCCTTCCAGCTGTCAGTGAATGGCTTATTGTCACCGTCTTGGGCTGAAA  
AAGAAACCTTC**TGA**TTACCTTCATGACGGAACCTAACGGACGAAGCCTACAGGGCAAGGG  
CCGCTTCGTATTCTGGAAGAAGGAAGGCATAGGCTTCGGTTTCCCCTCGGAAACTGCTTC  
TGCTGGAGGATATGTGTTGGAATAATTACGTCTGAGTCTGGGATTATCCGCATTGTATTTA  
GTGCTTGTAATAAAATGTTTGTAGTAACATTAAGACTTATACAGTTAGGGACA  
ATTAAAAAAA

## **FIGURE 120**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG  
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFC SALPAVT  
EMALFVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

**FIGURE 121**

TCCCGGACCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC  
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
GTGCCCCGGAACGAGTGGAAAGGCCCTGGCATCAGAGTGCAGCCCAGCACCTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCCTCGTGCCAGC  
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGGCTAC  
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACTTCACGGGTGC  
CCACTCAGGTCACTTATGGAACCCATGTCCATTGGCATCAGCTTCATGGCAACTACATGG  
ATCGGGTGCCACACCCCAGGCCATCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT  
CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TGA**GGCC  
CTGCTGATCCGCACCCATTCCCTCCCATGGCAAAACCCACTGTCTCCTCTCCA  
ATAAAGATGTAGCTC

## **FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYERGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

Signal peptide:

amino acids 1-20

## **FIGURE 123**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT  
 GACTCGCTGCTCGTGTCTGGTAGGCTATCTGGTCATCTGTGGCCAGG  
 ATGATGGTCTCCGGCTCAGAGGACCTGAGCGTGTGACACGAGGGCAGCCCCGGCC  
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAACGCCCAGGCCAATTCCACTCT  
 CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGCATTCTTGGCAGCCCCCAACCGCC  
 CGAACACAGCCCCCACCCAGCCAAGGTGAAGAAAATCTTGGCTGGGCAGCTTAC  
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTACAGGGAAAGATTGTGGACCATGGCAA  
 TGGGACCTTCAGCGTCCACTTCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
 TCGTCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
 GCCTCCAAAATCTCAACTGCCGGATGGAGTGGAGAAGGTAGAACGGGCCGGACCTC  
 GCTTGCACCCACGACCCAGCCAAGATCTGCTCCGAGACCACGCTCAGAGCTCAGCCACCT  
 GGAGCTGCTCCCAGCCCTCAAAGTCGTCTGTGTCTACATGCCCTTACAGCACGGACTAT  
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACATACCATAGTGATAACCCCTACTACCCATC  
 TGGG**TGA**CCCAGGGCAGGCCACAGAGGCCAGGGCTGGAAGGACAGGCCTGCCATGC  
 AGGAGACCATCTGGACACCAGGGCAGGGAAAGGGTTGGGCTCAGGCAGGGAGGGGGTGGAG  
 ACGAGGAGATGCCAAGTGGGCCAGGCCAAGTCTCAAGTGGCAGAGAAAGGTCCAAGTG  
 CTGGTCCAAACCTGAAGCTGTGGAGTGAATCACAGGAGCAGTGGAGGAGTGGCT  
 CTCTGTGCAGCCTCACAGGGCTTGCCACGGGCCAGAGAGATGCTGGGTCCCCGAGGCC  
 TGTGGCAGGCCGATCAGTGGCCAGATCAAGTCATGGAGGAAGCTAACGCCCTGGTT  
 CTTGCCATCCTGAGGAAAGATAGAACAGGGAGGGGAGATTCATCAGTGTGGACAGCCTG  
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCTAGGAGCCAGTCAGCAGGGTGGGTGGGC  
 CAGAGGAGCTCCAGCCCTGCCTAGTGGGCCCTGAGCCCTTGTGCTGAGCATG  
 GCATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTTGACAGATTGACCATCTGTCTC  
 CAGCCAGGCCACCCCTTCCAAAATCCCTTCTGCCAGTACTCCCCCTGTACCAACCCATT  
 GCTGATGGCACACCCATCCTTAAGCTAACAGACAGGACATTGTGGCCTCCACACTAAGGCC  
 ACAGCCCACCCATCCCGTGCTGTGTCCCTTCCACCCCAACCCCTGCTGGCTCCTCTGGAG  
 CATCCATGTCCCAGAGGGGCTCAACAGTCAGCCTCACCTGTCAGACACCAGGGTTCTCC  
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCAGA  
 GCATGTGCTGGATCTGTTCTGTGTCTGTGTGGGTGGGGAGGGAGGGAAAGTCTTGT  
 GAAACCGCTGATTGCTGACTTTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAGCTT  
 GCCCCGGGGCA

## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPKVVCVYIAFYSTDYRLVQKCPDYNHSDTPY
YPSG
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

## FIGURE 125

GTGAATGTGAGGGTTGATGACTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA  
 GGCAGGGCTGATTCTGGGCGGAGGAGTAGGGTAAAGGGTCTGCATGAGCTCCTTAAAG  
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGAGACTTGAACCAAGGCCACAGAAT  
 TGGTGGAAAGTGTGCGCGCCGCCGCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG  
 CATCTTCCCGAGCACCGGGATCCCGGGTAGGAGGCGACGCAGGGGAGCACCAGGCCAGCC  
 GGCTGCGGCTGCCACACGGCTCACC**ATG**GGCTCCGGCGCCGGCGCTGTCGCGGTGCCG  
 GCCGTGCTGCTGGTCTCACGCTGCCGGGCTGCCGTCTGGGACAGAACGACACGGAGCC  
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGCAGCTCGAACCCGGCACGGACTCCAAGG  
 GCTCCTCTCCTCCCCGCTGGGATATCGGTCCGGCGGCCAACCTCAAGGTGCGCTTCTCG  
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAAGACGCGCATCTTACTT  
 CGATCAGATCCTGGTGAATGTGGTAATTTTACATGGAGTCTGTCTTGTAGCACCAA  
 GAAAAGGAATTACAGTTCAAGTTTACGTGATTAAAGTCTACAGAGCCAAACTATCCAG  
 GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTGCGGGGACAAAGATGTTAC  
 TCGTGAAGCTGCCACGAATGGTGCCTGCTCACCTAGATAAAGAGGATAAGGTTACCTAA  
 AACTGGAGAAAGGTAAATTGGTGGAGGCTGGCAGTATTCCACGTTCTGGCTTCTGGT  
 TTCCCCCTA**TAG**GATTCAATTCTCCATGATGTTCATCCAGGTGAGGGATGACCCACTCCTG  
 AGTTATTGGAAAGATCATTTCATCATTGGATTGATGTTCTGGTTCTCATGGGTG  
 GATATGGATTCTAAGGATTCTAGCCTGCTGAACCAATACAAAATTCACAGATTATTGTG  
 TGTGTCTGTTCAAGTATTTGGATTGGACTCTAACGAGATAATACCTATGCTAAATGTA  
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCATTCCTGGATTACTGAATTAGT  
 TACAGATGTGAAATTATTGTTAGTTAAAGACTGGCAACCAGGTCTAAGGATTAGA  
 AAACTCTAAAGTTCTGACTTCATCACGGTTAGTGTGATACTGCCAAAGAACTGTACTG  
 TGTAAATATATTGATTATTTGTTTATTCTGGATTAGTTCTCTAAAGGTAAATGAA  
 TGGCTTGCCCACAAATTACCTTGACTACGATATCATCGACATGACTCTCTCAAAAAAAA  
 GAATGCTTCATAGTTGATTTAATTGTATATGTGAAAGAGTCATATTTCAGTTAAAGTTATATT  
 TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAGTTGCTTACCCAAAATCTAAG  
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTACCTTATTGC  
 TCAACTTAAATTAAATGATTGATAATAACCACCTTATTAAAAACCTAAGGTTTTTTTT  
 TCCGTAGACATGACCACTTTATTAACTGGTGGTGGGATGCTGTTCTAATTACCTAT  
 TTTCAAGGCTCTGTTGATTTGAAGTATCATCTGGTTGCCTTAACCTTAAATTGTA  
 TATATTATCTGTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTAGTGAATAT  
 CTTGTCTTGTATAGGTATATGAATTCAAAATTATTATGCTGTTATAGAATAAAGA  
 TTAATATATGTTAAAAAAA

## **FIGURE 126**

MGSRRALSAVPAVLLVLTPGLPVWAQNDTEPIVLEGKCLVVCDSPATDSKGSSSPLGI  
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIYFDQILVNNGNFFTLESVFVAPRKGIYSFSF  
HVIKVYQSQTIQVNLMNGKPVISAFAAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27

## FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTCGGCTGCGCCTCATTGCCTCGGGCCTGCGCTC  
GCCCTTTATGTCTTACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCGGAGC  
TTTCTTCTGGTTGGTGTCTACTGATTTCGTCCCTTGGTTCATGGCAAGAGTCATTA  
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTGGAGCGTTGTCTGTGTC  
TATATCCAAGAAATGTTCCGATTCGATATTATAAACTCTTAAAAAAAGCCAGTGAAGGTTT  
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTATGCGACTGCTGCCATGTTCTGGCT  
TGGGCTTGGAAATCATGAGTGGAGTATTTCTTGTGAATACCCATCTGACTCCTGGGG  
CCAGGCACAGTGGGCATTCATGGAGATTCTCCTCAATTCTCCTTATTCACTTGTGAC  
GCTGGTCATTATCTGCTGCATGTATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGA  
AAAAGTGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTAGCCCAGACCTTC  
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTATGGCAC  
CTGGGCATTCTTAGCTGCCGAAGCCTGAAACTCTGCCCTGCTGCCAAG  
ACAAGAACTTCTTACAACCAGCGCTCCAGATAACTCAGGAAACCAGCACTCCCAA  
ACCGCAGACTACATCTTAGAGGAAGCACAACGTGCCCTTTCTGAAAATCCCTTTCTG  
GTGGAATTGAGAAAGAAATAAAACTATGCAGATA

## **FIGURE 128**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLF
GIMSGVFSFVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKW
GILLIVLLTHLLVSAQTFISSLYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCQLCQDKN
FLLYNQRSR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## FIGURE 129

CGGCAACCAGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC**ATG**TTCGCTCTGGGCTGCCCTTCT  
 TGGTGCCTTGGCCTCGTCGAGAGCCATCTGGGGTTCTGGGCCAAGAACGTCAGCAGAAAGACGCC  
 AGTTGACCGCACCTACGTGGACGAGGTCAACAGCAGCTGGTCAACATCTACACCTCAACCATACTGTGACCC  
 GCAACAGGACAGAGGGCGTGCCTGTGTCAGCAGCTGGTCAACATCTACACCTCAACCATACTGTGACCC  
 TCCGCCAGAAGGAGGCTGTGGTCCTCCAGGTGCCCTAATCTGCAGGGATGTTCAGCGCAAGTACCTCT  
 ACCAAAAAGTGGAACGAACCCGTGTCAGCCCCCAACAAAGAATGAGTCGGAGATTCAAGTCTTCTACGTGGATG  
 TGTCACCCGTCAACAGCTAACACACATACAGCTCCGGTCAGCGCATGGACGATTGTGCTCAGGACTG  
 GGGAGCAGTTCAAGTCAACAGCAGCACAGCCCCAGTACTTCAGTCAAGTATGAGTCCCTGAAGGGTGGACT  
 CGGTAAATTGTCAGGTGACCTCAACAAGGCCCTCCCTGTCAGTCATCTCATTCAAGGATGTGCTGTGCT  
 TCTATGACCTGGACAACAACGTAGCCTCATCGGCATGTACAGACGATGACCAAGAAGGGGCCATACCGTAC  
 AGCGCAAAGACTCCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCCGGCT  
 CCCTGCTTCTACCCCTCGCAGAAGATGAACCGTCGATCAAGGGCACCGCAGAAAACCTGTCAAGTGTGG  
 TGTCAGTCAGCAGTCACGCTGAGGCATACGTCAAGTGGATGCTCTTGCCTGGTATATTCTCTCCTTTACC  
 TGCTGACCGCCTCCTGGCCTGCTGGGAGAACTGGAGGAGAAGAAGAAGACCTGCTGGTGGCATTGACCGAG  
 CCTGCCAGAAAGCGGTACCCCTGAGTCCTGGTCAATTCTGGCAGTCCCTTATGAGGGTTACAACCT  
 ATGGCTCCTTGAGAATGTTCTGGATCTACCGATGGTCTGGGTGACAGCGCTGGCACTGGGACCTCTTACG  
 GTTACCAAGGGCGCTCCTTGAAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTTGGAGGAGATG  
 ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCATTCCGACCAAGAACATACCTATGTCGCT  
 TGGCACGGAAAGGACAAGCGTGTCTCGGAAAAAGTACCCAGATCTACTTCTGAAACATTGCTGT  
 TCTATGCCCTCCTGTGGCAGCTGGTCACTTACCCAGACGGTGGTGAATGTCACAGGAAATCAGGACATCT  
 GCTACTACAACCTCCCTCGGCCAACCCACTGGCAATCTCAGCGCTTCAACAAACATCCTCAGCAACCTGGG  
 ACATCCTGCTGGGCTGCTTCTGTCATCATTGCAACAGGGAGATCAACCAACACGGGCCCTGCTGCGCA  
 ATGACCTCTGCCCCGTAATGTGGATCCCCAACACTTGGCTTCTACCCATGGCACAGCCGTGATGA  
 TGGAGGGCTGCTCACTGCTGCTATCATGTGCCCCAATATAACCAATTTCAGTTGACACATCGTTCATGT  
 ACATGATGCCGGACTCTGCATGTCAGCTACAGAAGCGGCACCCGGACATCAACGCCAGCGCTACAGTG  
 CCTACGCCCTGCCCTGGCATTGTCATCTCTCTGTGCTGGCGTGGCTTTGGCAAGGGAACACGGCGTTCT  
 GGATCGTCTCTCATCATTACATCGCACCCCTGCTCTCAGCACGAGCTCTATTACATGGGCCGGTGG  
 AACCTGGACTCGGGGATCTCCGCCATCCTCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGCC  
 TCTACGTGGACCGCATGGTCTGCTGGTCACTGGCAACGTCAACTGGTCGCTGGCTGCCTATGGGCTTATCA  
 TGCGCCCCAATGATTCGCTTCTACTTGTGGCATTGGCATCTGCAACCTGTCCTTACTTCGCCCTCTACA  
 TCATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATGTTGCACCTCCGTGG  
 GGGCTTCGCGCTCTCTCTTCCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAAGATGTCAGGGAGCACA  
 ACCGGGACTGCATCCTCTGACTTCTTGACGACCACGACATCTGGCACTCTCTCCATGCCATGTC  
 GGTCTTCTGGTGTGACACTGGATGACGACCTGGATACTGTGTCAGCGGGACAAGATCTATGTCCT**TAGC**  
 AGGAGCTGGGCCCTCGCTCACCTCAAGGGGCCCTGAGCTCTTGTGTCATAGACCGGTCACTCTGTCGT  
 GTGGGGATGAGTCCCAGCACCGCTGCCAGCACTGGATGGCAGCAGCACGCCAGGTCTAGCTTAGGCTTGG  
 GGGACAGCCATGGGTGCATGAAACCTTGCACTGGCCCTCTGCCAGGGAGCAGGCCCTGCTTGGCTCTCC  
 AGATGTTGGCAAATTGCTGCTTCTCTCAGTGTGTTGGGCCATTCCATGGGCCCTGCTTGGCTCTCC  
 GTCCCTTGTCAAGAGGAAGGATGGAAGGGACACCCCTCCATTTCTGCACTTGTGCACTTGGCT  
 ACAATGCCCGCAGGCTGGACCTCTTCCACTTCCACTCCACACTCCAGGGCTAGTCTGGGCC  
 ATCTCTGCTCTGTATCAGGGCCCCAGTTCTCTTGGGCTGTCCCTGGCTGCCATCACTGCC  
 AGGATGGATGGGGTATGAGATTGGGGTGGCCAGCTGGTGCCTAGGGCTGGCTCTTAGCAATGCGCT  
 CCTGGGGCAGTGCCTGATTCTCTCCCTCTGACCTGTGCTCAGGGCTGGCTCTTAGCAATGCGCT  
 AGGCCATTGAGAACCAGCCTCTGATTCAAGAGGCTGAATTCAAGAGGTGACCTCTTCCACTCAG  
 AGCCTCCAGTCTGCCCCAGTCTAGCCTGCTCTAGGACCCAGGGCTGGCTCTAAGTTCCG  
 AGTCTGTGTTAGTCATGCACACACATACCTATGAAACCTGGAGTTACAAAGAATTGCC  
 AGCAGCTGGGCCACCCCTGGTCTGGATCCCCCTCGTCCACCTGGCCACCCAGATGCTGAG  
 AGATGAGGTGGGTCTGGATCTTCTCAGAGCGTCTCCATGCTATGGTGCATTCC  
 GGGGCCCTGCTTTGGGATGGGAATGTGTTTTCTCCAAACTTGT  
 AGATGAGGTGGGTCTGGATCTTCTCAGAGCGTCTCCATGCTATGGTGCATTCC  
 GGGGCCCTGCTTTGGGATGGGAATGTGTTTTCTCCAAACTTGT  
 AGATGAGGTGGGTCTGGATCTTCTCAGAGCGTCTCCATGCTATGAATGAATT  
 TGCATTCAATAACACCAACAGACTCAAAAAAA

## **FIGURE 130**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pi: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFPCSVISIQDVLCPVYDLDNNVAFIGMYQTMTKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTLSDLVSQAVTSEAYVSGMLFCLGIIFLSFYLL
TVLLACWENWRQKKKTLVAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLDIDSDKNVIRTKQYLYVADL
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLIIILQREINHRALLRNDLCALECGIPKHGLFYAMGTALM
MEGLLSACYHVCPTYNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHHIATLLLSTQLYYMGRWKLDGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLYFAFYIIMKLRSGERI
KLIPLLICIVCTSVVWGFALFFFFQGLSTWQKTPAESREHNRDCIILDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDDTVQRDKIYVF

```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

**Leucine zipper pattern.**

amino acids 497-518

**N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

## FIGURE 131

GCTCAAGTGCCTGCCTGGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGGAGC  
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGCTGGCTGGAGGGCCTGTCCTG  
**ACCATG**TCCCTGCCTGGCTGTGGCTGCTTGTGTCTCCGTCCTGGCTGGAGGGCCTGTCCTG  
 CCAGCCTGCAGAGCTGTCTGGAAAGTCCAGAAAATATGGTGGAAATTCCCTTATACC  
 TGACCAAGTTGCCGCTGCCCGTGAGGGGGCTGAAGGCCAGATCGTGTCAAGGGACTCA  
 GGCAAGGCAACTGAGGGCCATTGCTATGGATCCAGATTCTGGCTTCTGCTGGTACCCAG  
 GCCCTGGACCGAGAGGAGCAGGCAGAGTACAGCTACAGGTACCCCTGGAGATGCAGGATG  
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTGTGACCGTGAAGGGATGAGAATGACCAGGTG  
 CCCCATTCTCTCAAGCCATCTACAGAGCTGGCTGAGCCGGGTACCAAGGCCTGGCATCCC  
 CTTCTCTTGCAGGCTCAGACGGGATGAGCCAGGCACAGCCAACCTCGGATCTCGAT  
 TCCACATCTGAGCCAGGCTCAGCCCCAGCCTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
 CTGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTGACCACGCCCTGGAGAGGAC  
 CTACAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAAGGCCTCAGGCCACCAGGCCACTG  
 CCACCGTGGAAAGTCTCCATCATAGAGACACCTGGGTGTCCTAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCCATACCCGCACCACATGGCCAGGTACACTGGAGTGGGGTATGTT  
 GCACTATCACCTGGAGAGCCATCCCCGGGACCCCTTGAAGTGAATGCAGAGGGAAACCTCT  
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG  
 AATTCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGACGTGCTGGTATGGATGAGAA  
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC  
 CAGGTACTGAAGTGAATGACTAGACTGTCAGCAGAGGATGCAGATGCCCGGCTCCCCAATTCC  
 CACGTTGTATCAGCTCTGAGCCCTGAGCCTGAGGATGGGTAGAGGGAGAGCCTTCCA  
 GGTGGACCCACTTCAGGCAGTGTGACGCTGGGGTGCTCCACTCGAGCAGGCCAGAAC  
 TCCTGCTCTGGTGTGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT  
 GAAGTCGAAGTCGCACTGAGATATCAATGATCACGCCCTGAGTTCATCACTCCAGAT  
 TGGCCTATAAGCCTCCCTGAGGATGGAGCCGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCGCCCTCCGCCTCATGGATTGCAATTGAGAGGGGAGACACA  
 GAAGGGACTTTGGCCTGGATTGGAGCCAGACTCTGGCATGTTAGACTCAGACTCTGCAA  
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGCAGAGTGTGGCGA  
 AGCTGGTGGGCCAGGCCAGGCCCTGGAGCCACGCCAGGTGACTGTGCTAGTGGAGAGA  
 GTGATGCCACCCCCCAAGTTGGACCAAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGC  
 AGCCGGCTTTCTGCTGACCATCCAGGCCCTCGACCCCATCAGCCGAACCTCAGGTTCT  
 CCCTAGTCATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGAGGTGCACACC  
 GCCCAGTCCTGCAGGGCGCCAGCCTGGGACACCTACACGGTGTGGAGGCCAGGA  
 TACAGCCCTGACTCTGCCCTGTGCCCTCCAAATACCTCTGCACACCCGCCAAGACCATG  
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGCACGGTCCCTACAGC  
 TTCACCCCTGGTCCAACCCACGGTGCACGGGATTGGCGCCTCCAGACTCTCAATGGTTC  
 CCATGCCTACCTCACCTGGCCCTGCATTGGTGGAGCCACGTGAACACATAATCCCCGTGG  
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCTGGTTGAGTGTGTCGCTGCAAC  
 GTGGAGGGCAGTGCATGCGCAAGGTGGCCGATGAAGGGCATGCCACGAAGCTGTCGGC  
 AGTGGGCATCCTGTAGGCACCCCTGGTAGCAATAGGAATCTCCTCATCCTCATTTCACCC  
 ACTGGACCATGTCAAGGAAGAAGGCCGATCAACCAGCAGACAGCGTGCCCTGAAGGCG  
 ACTGTC**TGA**ATGGCCCAGGCAGCTAGCTGGAGCTGGCCTCTGGCTCCATCTGAGTCCC  
 CTGGGAGAGAGGCCAGCACCAAGATCCAGCAGGGACAGGACAGAGTAGAAGCCCCCTCAT  
 CTGCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGTGAGGCCCTGGACACCAAC  
 TTTATGGACTGCCCATGGAGTGCTCCAAATGTCAGGGTGTGCCCCAATAATAAGCCCCA  
 GAGAACTGGCTGGCCCTATGGGAAAAAAAAAAAAAAAG

## FIGURE 132

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG  
KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLHVVKDENDQVP  
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPD MFQLEPRL  
GALALSPKGSTS LDHALERTYQLLVQVKDMGDQASGHQATATVEVSI IESTWVSLEPIHLAE  
NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN  
SHGEDYAAPLELHVLVMDENDNVPICPPRDPVT S IPELSPPGTEVTRLSAEDADAPGSPNSH  
V VYQLLSPEPEDGV EGRAFQVDPTSGSVTLGV LPLRAGQNILLV LAMDLAGAEGGFSSTCE  
VEVAVTDINDH APEFITSQIGPISLPEDVEPGTLVAMLTAIDADLEPAFRLMDFAIERGDTE  
GTFGLDWE PDSGHVRLRLCKNLSYEAPSHEVVVVVQSVAKL VGP GP GP GATATVTVLVERV  
MPPP KLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWL CIEKF SGEVHTA  
QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLC PRQDHGLIVSGPSKDPDLASGHGPYSF  
TLGPNPTVQRDWRLQTLNGSHAYLT LALHWV EPREHIIIPVVVSHNAQM WQLLVRVIVCRCNV  
EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFT HWTMSRKKD P QPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

## FIGURE 133

CCGGGGAC**ATG**AGGTGGATACTGTTCATGGGCCCTATTGGGCCAGCATCTGTGGCAA  
 GAAAAATTGGGACCAAGTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA  
 ATTGAGTCAACTAGTGAATTCAAACAATTGAAGCTCAATTCTGAAATCTCCCTCCT  
 TCAATCGGCCTGTGGATGTCCTGGTCCATCTGTCAGTCTGCAGGCATTAAATCCTCCTG  
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTAGACAATGA  
 AGATGATGAAATGCAACACAATTGAAGGGCAAGAACGGAGCAGTAATAACTCAACTACGGGG  
 CTTACCATTCCCTGAAAGCTATTACACGAGATGGACAACATTGCCGCAGACTTCCTGAC  
 CTGGCGAGGAGGGTGAAGATTGGACATTGTTGAAAACCGGCCATGTATGTACTGAAGTT  
 CAGCACTGGGAAAGGCCTGAGGCGGCCGGCTTGGCTGAATGCAGGCATCCATTCCCGAG  
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACAGAGG  
 GATCCAGCTATCACCTCCATCTGGAGAAAATGGATATTTCTTGTGCTGGCCAATCC  
 TGATGGATATGTGTACTCAAACCTCAAACCGATTATGGAGGAAGACGCCGTCGGAAATC  
 CTGGAAAGCTCCTGCATTGGTCTGACCCAAATAGAAACTGGAACGCTAGTTTGCAAGGAAAG  
 GGAGCCAGCGACAACCCTGCTCCGAAGTGTACCATGGACCCCAGCCAATTGGAAGTGGA  
 GGTGAAATCAGTGGTAGATTTCATCCAAAACATGGAATTCAAGGGCTTCATGACCTGC  
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGTACTCAGTCAAAAGGCCAGATGCC  
 GAGGAACTCGACAAGGTGGCGAGGCTGCGGCCAAAGCTCTGGCTCTGTGTCGGCACTGA  
 GTACCAAGTGGTCCCACCTGCACCACTGTCTATCCAGCTAGCAGGGAGCAGCATGACTGGG  
 CGTATGACAACGGCATCAAATTGCAATTGCAATTGAGGTTGAGAGATAACGGGACCTATGGC  
 TTCCCTCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGCTGAAGAC  
 CATCATGGAGCATGTGCGGGACAACCTTAC**TAG**GCGATGGCTGCTCTGTACATTAT  
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTTCTACCTGTGAG  
 TCAGAGCCCTCTGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCGGAGT  
 CGTGTGCTCTGGCGGTGCCCCGCAAGAAACTGTTCTGCCAGCCTGCTCAATTGGTCTG  
 CTGTTTTGATGAGCCTTGTCTGTTCTCCCTCACCTGCTGGCTGGCGGCTGCACTC  
 AGCATCACCCCTCCTGGTGGCATGTCCTCTACCTCATTTAGAACCAAAGAACATC  
 TGAGATGATTCTACCCCTACACATCTAGCCAAGCAGTGACCTGCTCTGGGGCACT  
 GTGGGAGACACCAACTGTCTTAGGTGGTCTCAAAGATGATGAGTAAATTCTTTAATTTC  
 TCGCAGTCTCCTGGAAAATATTCTGAGCAGCAAATCTGTAGGGATATCAGTGAAG  
 GTCTCTCCCTCCCTCTGTTCTGTTTTTTGAGACAGAGTTGCTCTGTTGCTCTG  
 CAGGCTGGAGTGTGATGGCTCGATCTGGCTCACACACCTCTGCCCTGGGTTCAAGCA  
 ATTCTCCTGCCTCAGCCTCTGAGTAGCTGGTTATAGGCGCATGCCACCATGCCCTGGCTA  
 ATTGTTGTTTTAGTAGAGACAGGGTTCTCCATGTTGGCTAGGCTGGCTCAAACCTCC  
 ACCTCAGGTGATCTGCCCTCTGGCTCCCAGAGTGTGGATTACAGGTGTGAGCCACTG  
 TGCCGGGCCGTCCCTCTTTAGGCCTGAATACAAAGTAGAACATCACTTCCCTCAC  
 TGTGCTGAGAATTCTAGATACTACAGTTACTCCTCTTCCCTGTTATTCAAGTGTG  
 ACCAGGATGGCGGGAGGGATCTGTGCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA  
 GTGACCACATAATTGCAAGGATGGTAAATTACCCATCTGTCTTAATGGGCTTACCTCCT  
 CTTGCCTTTGAACACTCAAAGATCTAGGCCTCATCTTACAGGTCTAAATCACTCAT  
 CTGGCCTGGATAACTCACTGCCCTGGCACATTCCATTGTCAGTGTGGTATCCTGTGTT  
 TCCCTGTCTGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG  
 TCTGTCTATTGTTGATCCTGGACCAAGTTCTAAAGTAGAGCAAGAACATTCAACCA  
 GCCTCTGTTCATTCACCTCAGCACGTACCATCTGCTCTTGTGTTGTTGTTGTT  
 TTGTTTTGCTTTACAAACATGTCTGAAATCTAACCTCCTGCCAGGATTGACA  
 GCATCTGGTGTGCTTATAAGCCAATAATATTCAATGTGAAAAAAAAAAAAAA

## **FIGURE 134**

MRWILFIGALIGSSICGQEKFQGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR  
PVDVLVPSVSLQAFKSFLRSQGLEYAVTIEDLQALLDNEDDEMQHNEGOERSNNFNYGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKVRRPAVWLNAGIHSREWI  
SQATAIWARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS  
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY  
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDNLY

**Signal peptide:**

amino acids 1-16

## **FIGURE 135**

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTGTTCCAAA**ATG**  
 GCATCTTACCTTATGGAGTACTCTTGCTGTGGCCTCTGTGCTCCAATCTACTGTGTGTC  
 CCCGGCCAATGCCCCAGTGCATAACCCCCGCCCTCCTCCACAAAGAGCACCCCTGCCTCAC  
 AGGTGTATTCCCTCAACACCGACTTGCCTCCGCCTATACCGCAGGCTGGTTGGAGACC  
 CCGAGTCAGAACATCTCTCCCTGTGAGTGTCTCCACTCCCTGGCCATGCTCTCCCT  
 TGGGGCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTAACCTCACACACA  
 CACCAGAGTCTGCCATCCACCAGGGCTCCAGCACCTGGTCACTCACTGACTGTTCCCAGC  
 AAAGACCTGACCTTGAAGATGGAAAGTGCCCTTCGTCAAGAAGGAGCTGCAGCTGCAGGC  
 AAATTTCTTGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTCTACAGATTCTCCA  
 ACCCCTCCATTGCCAGGCAGGATCAACAGCCATGTGAAAAAGAACCCAAGGGAAGGTT  
 GTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCATGGTCTGGTAATCACATTCTT  
 TAAAGCCAAGTGGAGAAGCCCTTCACCTTGAATATAAGAAAGAACTTCCATTCTGG  
 TGGCGAGCAGGTCACTGTGCAAGTCCCCATGATGCACCAGAAAGAGCAGTCGCTTTGGG  
 GTGGATACAGAGCTGAAGTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTT  
 CTTGTCCTCCCTAGCAAGGGCAAGATGAGGCAACTGGAACAGGCCTGTCAGCCAGAACAC  
 TGATAAAAGTGGAGCCACTCACTCCAGAAAAGGTGGATAGAGGTGTTCATCCCCAGATTTC  
 ATTCTGCCTCCTACAATCTGAAACCATCCTCCGAAGATGGCATCCAAAATGCCTTGA  
 CAAAAATGCTGATTTCTGGAATTGCAAAGAGAGACTCCCTGCAGGTTCTAAAGCAACCC  
 ACAAGGCTGTGCTGGATGTCAGTGAAGAGGGCACTGAGGCCACAGCAGCTACCACCAAG  
 TTCATAGTCGATCGAAGGATGGTCCCTCTTACTTCAGTGTCTCCTCAATAGGACCTTCC  
 GATGATGATTACAATAAGCCACAGACGGTATTCTCTTCTAGGGAAAGTGGAAAATCCCA  
 CTAATCC**TAG**GTGGAAATGGCCTGTTAACTGATGGCACATTGCTAATGCACAAGAAATAA  
 CAAACCACATCCCTCTTCTGTTCTGAGGGTGCAATTGACCCCAGTGGAGCTGGATTCGCTG  
 GCAGGGATGCCACTCCAAGGCTCAATCACCAACCATCAACAGGGACCCAGTCACAAGCC  
 AACACCCATTAACCCAGTCAGTGCCTTTCCACAAATTCTCCAGGTAACTAGCTTCATG  
 GGATGTTGCTGGTTACCATATTCCTGAGGGCTCCAGGAATGGAAATACGCCAAC  
 CCAGGGTAGGCACCTCTATTGAGAATTACAATAACACATTCAATAAAACTAAAATATGAAT  
 TCAA  
 AAAAAAA

## **FIGURE 136**

MASYLYGVLFAGVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFPVSVSTSLAMSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP  
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK  
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
GVDTELNCFVLQMDYKGDAVAFFVLPSPKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF  
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

## FIGURE 137

GGCTGACCGTGCTACATTGCCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGC  
 CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAG  
 CCTTATCTCTCACCTTCAAGTCCCCTTCTCAAGAACATCCTGTCTTGCCTCTAAAG  
 TCTTGGTACATCTAGGACCCAGGCATCTTGCTTCCAGGCCACAAAGAGACAGATGAAGATGC  
 AGAAAGGAAATGTTCTCCTATGTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCC  
 AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC  
 CACCAACTCTGGGCCAGTGTGACCTCCAGTGGGTCAAGCACAGCCACCATCTCAGGGTCCA  
 GCGTGCACCTCCAATGGGTCAAGCATAGTCACCAACTCTGAGTCCATACAAACCTCCAGTGGG  
 ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCAGTGGGATCAGCATAGCCACCAA  
 CTCTGAGTCCAGCACAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC  
 CCTCCAGTGGGCCAGCACAGTCACCAACTCTGGTCCAGTGTGACCTCCAGTGGAGCCAGC  
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCAGTGCACCAACTCTGA  
 GTCTAGCACACTCTCCAGTGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACCTCCA  
 GTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGGCCAGCACAGCC  
 ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCAGTGCACCAACTCTGAGTCCAG  
 CACAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGG  
 CTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCCAGCACAGCCACCAAC  
 TCTGACTCCAGCACAGTGTCCAGTGGGCCAGCAGTGCACCAACTCTGAGTCCAGCACGAC  
 CTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCTAGCA  
 CAGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCGGCACAGCCACCAACTCTGAG  
 TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCCAG  
 TGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCAACACAGCCA  
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGCCAGCAGTGCACCAACTCTGAGTCCAGC  
 ACAACCTCCAGTGGGTCAAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGG  
 TAGCACAGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACT  
 CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAAAC  
 TCCAGTGGGCCAACACAGCCACCAACTCTGGTCCAGTGTGACCTCTGCAGGCTTGGAAC  
 AGCAGCTTGACTGGAATGCACACAACCTCCATAGTGCATCTACTGCAGTGAGTGAGGCAA  
 AGCCTGGTGGTCCCTGGCGTGGAAATCTCCTCATCACCTGGTCTGGTTGGCG  
 GCCGTGGGCTTTGCTGGCTCTTCTGTGAGAAACAGCCTGTCAGGAGACAGCAGGAGACAGTA  
 GGAATCATGGAGCCCCCAGGCCAGGTGGAGTCCTAACAGGTTCTGGAGGAGACAGTA  
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCCCTGAAGCAGCCGGAAAGCAAG  
 TGCCGCATTCTCAGGAAGGAAGAGACCTGGCACCCAAAGACCTGGTTCTTCTTCATTCTAC  
 CCAGGAGACCCCTCCAGCTTGTGAGATCCTGAAATCTTGAAGAAGGTATTCTCACC  
 TTTCTGCCTTACAGACACTGGAAAGAGAAATCTATATTGCTCATTAGCTAAGAAATAA  
 ATACATCTCATCTAACACACAGACAAAGAGAAGCTGTGCTTGGCCGGGTGGTATCTAG  
 CTCTGAGATGAACTCAGTTAGGAGAAACCTCCATGCTGGACTCCATGGCATTCAAAA  
 TCTCCACAGTAAAATCCAAAGACCTCAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAA

## **FIGURE 138**

MKMQKGNVLLMFGLLHLEAATNSNETSTSANTGSSVISSGASTATNGSSVTSSGVSTATI  
SGSSVTSGSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTSSGASTATNSE  
SSTPSSGASTVTNGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
TTSSGASTATNSESSTSSGASTATNSESSTVSSRASTATNSESSTSSGASTATNSESRTT  
SNGAGTATNSESSTSSGASTATNDSSTVSSGASTATNSESSTSSGASTATNSESSTTSS  
GASTATNDSSTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA  
NTATNSESSTVSSGASTATNSESSTSSGVSTATNSESSTSSGASTATNDSSTTSEAST  
ATNSESSTVSSGISTVTNSESSTSSGANTATNGSSVTSAGSGTAALTGMHTTSHSASTAV  
SEAKPGGLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP  
GPGGNHGAPHRPRWSPNWFWRPVSSIAMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

**FIGURE 139**

GGGAGAGAGGATAAAATAGCAGCGTGGCTCCCTGGCTCCTCTGCATCCTTCCCACCTTC  
CCAGCAATATGCATCTGCACGTCTGGTCGGCTCCTGCTCCCTCCTCTGCTACTGGGGGCC  
CTGTCTGGATGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
GCTGAGCAATGCAGAGAGAGAGGTGGCAAGGCCCTGGATGGCATCAACAGTGGAAATCACGC  
ATGCCGGAAGGGAAAGTGGAGAAGGTTTCAACGGACTTAGCAACATGGGAGCCACACCGGC  
AAGGAGTTGGACAAAGGCGTCCAGGGCTCAACCACGGCATGGACAAGGTTGCCATGAGAT  
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGTCAACAACG  
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTCCACACTGGGTCCAC  
CAGGCTGGGAAGGAAGCAGAGAAACTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGG  
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC  
TGCAGAATGCTCATAATGGGTCAACCAAGCCAGCAAGGAGGCCAACAGCTGCTGAATGGC  
AACCATCAAAGCGGATCTCCAGCCATCAAGGAGGGCCACAACCACGCCGTTAGCCTCTGG  
GGCCTCAGTCACACGCCCTTCATCAACCTTCCGCCCTGTGGAGGAGCGTCGCCAACATCA  
TGCCCTTAAACTGGCATCCGGCCTTGCTGGAGAATAATGTCGCCGTTGTACATCAGCTGAC  
ATGACCTGGAGGGTTGGGGTGGGGACAGGTTCTGAAATCCCTGAAGGGGGTTGTACTG  
GGATTGTGAATAAACTTGATACACCA

## **FIGURE 140**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLQGVNHAADQAGKEVEKLQGAHAAAGQAGKELQN
AHNGVNOASKEANOLLNGNHNQSGSSSHOGGATTPLASGASVNTPFINLPALWRSVANIMP
```

### Important features of the protein:

### Signal peptide:

## amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

## FIGURE 141

CTCCGGGTCCCCAGGGGCTGCGCCGGGCGCTGGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC  
 CCCGGGGGGCGATGACCCTGCGCTGACCTGACTCACTCCAGGTCGGAGGGGGCCCCGGGGCAGCTCG  
 GGGCGGACCGCGGGCGGAGCTGCCGCCGTGAGTCGGCCGAGCCACCTGAGCCCCGAGCCGCGGGACACCGTC  
 GCTCCTGCTCTCGA**ATG**CTGCGCACCGCGATGGGCTGAGGAGCTGGCTCGCCGCCCATGGGCGCTGCC  
 CCTCGGCCACCGCTGCTGCTCCTGCTGCTGCTCCTGCTGAGCCGCCCTCGACCTGGCGCTCAGC  
 CCCCGATCAGCCTGCCCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGAAGCTGAACACATCTCAACTAC  
 ACAGCCCTCTGCTGAGCAGGGATGGCAGGACCTGTACGTGGGTGCTGAGAGGCCCTCTTGCACTCAGTAGC  
 AACCTCAGCTTCTGCCAGCGGGAGTACCAAGGAGCTGCTTGGGTGAGACAGCAGAGAAACAGCAGTGC  
 AGCTTCAAGGGCAAGGACCCACAGCGCAGCTCAAAACTACATCAAGATCCTCTGCCGCTCAGCAGTCAC  
 CTGTTACACTGTCAGCAGCCTCAGCCCCATGTGACCTACATCAACATGGAGAACTTCACCTGGCAAGG  
 GACGAGAAGGGAAATGTCTCTGGAAGATGGAAGGGCGTTGTCCTCTGACCCGAATTCAAGTCCACTGCC  
 CTGGTGGTTGATGGCAGCTACACTGGAACAGTCAGCAGCTCCAAGGGAAATGACCCGCCATCTCGCGGAGC  
 CAAAGCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTGTCAGCAGACTGCC  
 ATTCCCTGAGAGCCTGGCAGCTTGAAGGCGATGATGACAAGATCTACTTTTCTCAGCAGACTGCCAGGAA  
 TTTGAGTTCTTGAGAACACCATTGTGTCCTGCATTGCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG  
 CTACAGCAGCGCTGGACCTCCTCAAGGCCAGCTGCTGTGCTCACGCCAGCAGATGGCTTCCCTCAAC  
 GTGCTGAGGATGTCTCACGCTGAGCCCAGCCCCAGGACTGGCGTGCACCCCTTTCTATGGGTCTTCAC  
 TCCCAAGTGGCACAGGGAAACTACAGAAGGCTGCGCTGTGCTCTCACATGAAGGATGTGCAAGAGACTCTC  
 AGCGGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCACACCCGG  
 CCTGGAGCGTGCATCACCAACAGTGGCGGGAAAGGAAGATCAACTCATCCTGCAAGCAGCCAGGCTGCTG  
 AACCTCCTCAAGGACCACTTCTGATGGACGGCAGGTGCGAAGCCGATGCTGCTGCAAGCCCCAGGCTGCG  
 TACCAAGCGCTGGCTGTACACCGCTCCCTGGCGTGCACACACTACGATGTCCTCTCAGTGGGACTGGTGC  
 GGCGGCTCCAACAGGCAAGTGGAGGCTGG  
 CAGCCCGTGAGAACATGCTCCTGGACACCCACAGGGGCTGCTGTATGCCGCTCACACTCGGGCTAGTCCAG  
 GTGCCCATGGCAACTGCAAGCCTGTACCGGAGCTGTGGGACTGCCCTCGCCGGGACCCCTACTGTGCTTG  
 AGCGGCTCCAGCTGCAAGCACGTCAAGCTCAGCCTCAGCTGGCCACCAGGCCGTGGATCCAGGACATCGAG  
 GGAGCCAGGCCAACGGACCTTGCAGCGCTCTCGGTTGTGTCCTCGTCTTGTACCAACAGGGAGAACCCA  
 TGTGAGCAAGTCCAGTCCAGCCAACACAGTGAACACTTGGCTGCCGCTCTCCTCCAACCTGGGACCCGA  
 CTCTGGCTACCGAACGGGCCCCCTCAATGCCCTGCCCTGCCACGTGCTACCCACTGGGACCTGCTGCTG  
 GTGGGCAACCAACAGCTGGGGAGTTCCAGTGTGGTCACTAGAGGAGGGCTCCAGCAGTGGTAGCCAGCTAC  
 TGCCCAGAGGTGGTGGAGGACGGGGTGGCAGACCAAACAGATGAGGGTGGCAGTGTACCCGTATTATCAGCACA  
 TCGCGTGTGAGTGCACCAAGCTGGCAAGGCCAGCTGGGTGCAAGACAGGTCTACTGGAAAGGAGTTCTGGTG  
 ATGTGACGCTTTGTGCTGGCGTGTGCTCCAGTTATTCTGCTCTACCGGCACCGAACAGCATGAAA  
 GTCTTCTGAGCAGGGGAATGTGCCAGCGTGCACCCCAAGACCTGCCCTGTGGTGCTGGGGCTGAGACCCGC  
 CCACTCAACGCCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAAGTCCCTGTCAGACAGCCCCCG  
 GGGGCCGAGTCTCACTGAGTCAGAGAACAGGCCACTCAGCATCCAAGACAGCTCGTGGAGGTATCCCCAGTG  
 TGCCCCCGGCCCCGGGTCCGCCCTGGAGATCCGTGACTCTGTGGTGT**TGA**AGAGCTGACTTCCAGAGGACG  
 TGCCCTGGCTCAGGGGCTGTGAATGCTGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTCGTGGAAAC  
 ACGACCGTGGCCGGGGCTTGGAGCCAGCTGGCTGCTCTCCAGTCAAGTAGCGAAGCTCC  
 TACCAAGGACACCCAAACAGCCCTGG  
 CAGTGTCTTATGTAACAGGCCCTTGTGTTAAAAAAACATTCAAATGTGAAACTAGAAATGAGAGGGAGAG  
 ATAGCATGGCATGCAAGCACACAGCGCTGCTCCAGTTCATGGCTCCAGGGGCTGTTGGGATGCATCAAAGTGG  
 TTGCTGAGACAGAGTTGAAACCCCTACCAACTGGCCTTTCACCTTCCACATTATCCCGCTGCCACCGGCTGC  
 CCTGTCTCACTGCAAGATTCAAGGACAGCTTGGCTGCGTGTGCTGCACTCAGCCGAGGGATGTAGTTG  
 TTGCTGCCGTGCTCCCACCCACCTCAGGGACCAAGAGGGCTAGGTGGCACTGCCGCCCCCCTACCCAGGTCTGGGCTC  
 GGACCCAACCTCTGGACCTTCCAGCGTATCAGGCTGTGGCCACACGAGAGGACAGCGCGAGCTCAGGAGAGA  
 TTTCGTGACAATGTACGCCCTTCCCTCAGAATTCAAGGGAGAGACTGTGCGCTGCCCTCCCGTTGCGTGA  
 GAACCCGTGTGCCCTTCCCACCATATCCACCCCTCGCTCCATTTGAACCAAACAGCAGGAAACTAAGTGCACC  
 CTGGTCTCTCCCCAGTCCCCAGTTCAACCTCCATCCCTCACCTCCTCCACTCTAAGGATATCAAACACTGCC  
 AGCACAGGGGCCCTGAATTATGTTTATACATTAAAGATGCACTTATGTCATTAAATAAA  
 GTCTGAAGAATTACTGTTAAAAAA

## FIGURE 142

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962  
><subunit 1 of 1, 837 aa, 1 stop  
><MW: 92750, pI: 7.04, NX(S/T): 6  
MLRTAMGLRSWLAAPWGALPPRPLL LLLL LLLL QPPPPTWALSPRISLPLGSEERPFLRF  
EAEHISNYTALLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKG  
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP  
FDPNFKSTALVVDGELYTGTVSSFQGNDPAISRSQSLRPTKTESSLNLQDPAFVASAYIPE  
SLGSLQGDDDKIYFFFSETGQEFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC  
SRPDDGFPFNVLQDVFTLSPSPQDWRTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG  
LYKEVNRETQQWYT VTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR  
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRHLKAVSVGPRVHIIIEELQIFSSGQ  
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVS LYQP  
QLATRPWIQDIEGASA KDLCSASSVVSPSFVPTGEKPCEQVQFQOPNTVNTLACPLLSNLATR  
LWLRLNGAPVN ASASCHVLPTGDL L L VGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ  
TDEGGSPVIIISTS RVSAPAGGKASWGADRSY WKEFLVMCTLFVLAVLLPVL FLLYRHRNSM  
KVFLKQGECASVHPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFT ESEKR  
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

## FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCAGCGGGCGCCGGCTACGAAGAGGACGGGGACAGGCCTGCGAACCGA  
 GCCCAGCCAGCCGGAGGACGCCAGGGCGGGACGGGAGCCCCGGACTCGTCTGCCGCCGCTCGCCGTC  
 TGCCGGCCCCCGTCCCCCGCGCGAGCGGGAGGAGCCGCCACCTCGCCGCCAGCCGCCCTAGCGCGC  
 CGGCATGGTCCCCTCTTAAAGGCCAGGCCGGCGGGGGCGGTGTGCCAACAAAGGCCGCCGGCTAGCGCG  
 CCTGCCGGCGCTCGGGGCCGATGGCGCGGGCCCGGGCGCTGCCGCCAGCCGCCCTGCCGCCGGCTCG  
 CGCGCTAGGCCGGCTGCCCTCCGTGGCGGGGAGCGGGCTGAGGGCGCGGCCAGCCCTGCCGCCGG  
 GGCGCGGCCGGCGGCCGGCGAGCGGCCGGCAGTGGCGCGGCCGGCTAGCGTGC  
 TGCTCGGGCTCGTCTGGCTCGTGTGCCCTCGCGGCTCGTCTGCCGCCGGCTTCCGAGCTGAAGCGAGCG  
 GCCCACGGCGCCGCCAGCCCGAGGGCTGCCGGCTGCCGCCAGGCCGCCCTCCCAGGCCGCCGCC  
 GCGATGCCGCCGGGCGCAGCTCGGCCGCCGCTGCCGCCAGATGGCGGCCGCCAGAGAACTTCTCT  
 TCGTGGAGTCATGACCCCCAGAAATACCTGCAGACTCGGCCGTGCCGCCACAGAACATGGTCCAAGACAA  
 TTCTGGAAAGTTCAAGTCTCTCAAGTGAGGGTCTGACACATCTGTACCAATTCCAGTAGTGCACACTACGGG  
 GTGTGGACGACTCCTACCCGCCAGAAGAACGATCCTTCATGATGCTCAAGTACATGCACGACCAACTTGGACA  
 AGTATGAATGTTTATGAGAGCAGATGACGTGTACATCAAAGGAGACGCTGGAGAACTTCTGAGGAGTT  
 TGAACAGCAGCGAGCCCCCTTTCTGGCAGACAGGCCCTGGCACCGAAAGAAATGGAAAATGGCCCTGG  
 AGCCTGGTGAGAACTTCTGCATGGGGGGCTGGCGTATGAGCCGGAGGTGCTTCGGAGAATGGTGC  
 ACATTGGCAAGTGTCTCGGGAGATGTACACCACCATGAGGACGTGGAGGTGGAAGGGTGTCCGGAGGTTG  
 CAGGGGTGCAGTGTCTGGTCTATGAGATGCCAGCTTTTATGAGAAATTAGAGCAGAACAAAAGGGT  
 ACATTAGAGATCTCCATAACAGTAAACAGTACATTACACCCAAACAAAACCCACCCCTACCAAGT  
 ACAGGCTCCACAGTACATGCTGCCAGAAGATATCCGAGCTCCGCCATGCCACAATACAGCTGCACCGCG  
 TTGCTCTGATGAGCAAATACAGCAACACAGAAATTCTAAACAGGACCTCCAGTGGGAATCCCTCCCTTC  
 TGAGGTTTCAGCCCCGCCAGCGAGGAGATTCTGGAATGGAGTTCTGACTGGAAATCTGAGGAGC  
 TTGACGGCCAGCCCCCTCGAAGAGGAATGGACCTCCGCCAGGGAGCCTTGAGCAGACATTGT  
 TGGAGATGATCAATGCCAACCGCAAGACCGAGGGCGCATATTGACTCTAAAGAGATCCAGTACGGCTACCG  
 GGGTAACACCCATGTATGGGCTGAGTACATCTGGACCTGCTCTGTACAAAAGCACAAAGGGAAAGAAA  
 TGACGGTCCCTGTGAGGAGGCACGCTTACAGCAGACTTCAGAAATCTGGATCTGTCTCTCTCAA  
 ACTCCCTGAAGAAGCTCCCTTCAAGTACCCCTAAAGCCGACATGCAGATTTCGCTGTGCTGGAG  
 GAGATTACCGCATTAAAGTACCCCTAAAGCCGACATGCAGATTTCGCTGTGCTGGAG  
 CCCTGGAAGTAGGATCTCCAGTTAACATGAATCTTGCTCTCTGCGACGTCGACCTCGTTACTA  
 CAGAATTCTCAGCGATGTCGAGCAAATACAGTTCTGGCCAACAAATATATTTC  
 CAAATCATCTCAGCCAGTATGACCCAAAGATTGTTATAGTGGAAAGTCTCCAGTGACAACC  
 ATTGCTCTTACTCAGAAAACGGCTTCT  
 GGAGAAACTATGGTTGGCATCACGTGATTATAAGGGAGATCTGTCGAGTGGGTGCTTGT  
 GATGTTCCA  
 TCCAAGGCTGGGGCTGGAGGATGTGGACCTTCAACAAGGTTGTCAGGAGGTTGAAGACGTTAGGAGCC  
 AGGAAGTAGGAGTAGTCCACGTCACCATCTGTCCTTGTGATCCAATCTGACCCAAACAGTACAAAATGT  
 GCTTGGGGTCCAAGCATTGACCTATGGGTCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAAATGATCCA  
 GTTACAGTAAAGCAGCAATAATAATGGCTCAGTGGACAGCC  
 TAA  
 GTCCAGCTTGCTGGAAAAGACGTTT  
 TAATTATCTAATTATTTCAAAATTTTGTATGATCAGTTTGAGCTTGAAGTCCTGATACAAGGATATATT  
 AACGTGGTTCTTACATAGGACTCTTAAAGATTGAGCTCTGAAACAAGAAGGTGATCAGTGGCTTTGAA  
 CACATCTCTGCTGAACATTATGTCAGACCTGCTTAACCTTGACTTGAAATGTACCTGATGAACAAA  
 ATT  
 TTTAAAAAAATGTTTCTTGTGAGACCTTGTCTCCAGTCTATGGCAGAAAACGTTGAA  
 CACATTCCACAGATTCTACCTTTGT  
 TATTGTAACAAAACACTGTAACCTGTTAAATGTTCTGTTGAGTTGTTAACATT  
 CCACAGATTCTACCTTTGT  
 GTTTGTTTTTTTACAATTGTTAAAGCCATTTCATGTTCAAGTAA  
 GAGAAGGAAATGTGATAATA  
 GCTGTTTCATCATTGTCAGGAGAGCTTCCAGAGTTGATCATTCTCTCATGGTACTCTGCTCAGCATGG  
 CACGTAGGTTTTGTTGTTGTTGTTCTTTGAGACGGAGTCTCAGCTGTTACCCAGGCTGGAATG  
 CAGTGGCGCAATTGGTCACCTTAACCTCCACTCCCTGGTCAAGCAATTCCCTGCCCTTGCC  
 AGT  
 AGCTGGGATTACAGGCACACACCACGCCAGNTAGTTTTGTATT  
 TTAGAGAGACGGGGTTACCAT  
 GCAAGCCCAGTGGCACGTTAAAGCAAGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG  
 TGGTAGTTCATCGGCCAAATAGACCTGGCATTAAATTCAAGAAGGATTGCA  
 CTCTTAAAGGGAAAATATTAAATGTTAGAATGACAAAGATGAATT  
 ATTACAATAATCTGATGTACACAGACT  
 GAAACATACACACATACACCCCTAATCAAACGTTGGGGAAAATGT  
 ATTGTTGTTGAGATGGTTCTTCAAGACGCTCTGCCATTCTGAGTACCTGTTAGT  
 TAGTATTATTATGTTGATCGG  
 GAGTGTGTTAGTCTGTTATTGCAAGAACCGATCTCCAAAGATT  
 CCCTGGAAACGCTTTCCCCCTCC

**FIGURE 143B**

TTAATTTATATTCTTACTGTTACTAAATATTAAGTGTCTTGACAATTGGTGCATGTGTTGGG  
GACAAAAGTGAATGAATCTGTCATTATACCAAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTGTT  
TTCATTTAGATTCAAACAGTGATAGACTGCCATTAAATACACGTCATTGGAGGGCTGCGTATTGTAAATAG  
CCTGATGCTCATTGGAAAAATAAACAGTGAACAATATTTCTATTGACTTTGAACCATTGTCTCATT  
ATTCCCTGTTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAACTAAACACGAAAAAA

**FIGURE 144**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836  
><subunit 1 of 1, 802 aa, 1 stop  
><MW: 91812, pi: 9.52, NX(S/T): 3  
MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKAGPRRRASPEGCRSGQAAASQAGGAR  
GDARGAQLWPPGSDDPGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTI PGKVQFFSSEG  
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLENFLR  
SLSNSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT  
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP  
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFQPRQREE  
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY  
GYRRVNPAMYGAEYILDLLLLYKKHKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR  
INQESGSLSFLSNSLKKLVPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC  
LIPNQNVKLVVLNFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ  
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT  
QKTGFWRNYGFGITCIYKGDLVRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH  
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

**Signal peptide:**

amino acids 1-23

## FIGURE 145

GGACAACC GTT GCT GGG GTCCC AGGG C CT GAGG CAGG AC GG T AC TCC G CT GAC AC CCT TCCC  
 TT C GGC CT T GAGG T TCCC AGC CT GGG CCC AGG AC GGT CC GG T CG AT GG CAG AGT GCT  
 AC GG AC GAC GC CT **ATGA** AGC CCT T AGT C CT T AGT GCG CT T T GCT AT GG C CT T CG T CT G  
 TG C CG G CT T AT C CG AGC AT A CT GT GAC AC CT GAT G AAG AGC AAA ACT TGA AT CATT ATATA  
 CAAG TTT AGAG A ACCT AGT ACG AAGT GTT CCCT GGG GAGC CAGG T CG T GAG AAAA ATC  
 TAA CT CT CAAA ACAT GTT ATT CT ATAG C AT CAA AGG AT CAA AAT T AAGG AGC T AGT TA  
 CAC AT GGAG AC GCT TCA CT GAGA AT GAT GTT TAAC CA AT CCT AT CAGT G AAG A AACT A CA  
 ACT TT CCCT ACAGG AGG CTT CACAC CGG AA ATAGG AA AG AAAA ACAC AC CGG AA AGT ACCC  
 ATT CT GG T CG AT CAA ACC AA CA AT GTT CCATT GTT G CAT G CAG AGG A ACCT T AT ATT G  
 AAAA TGAAG AGCC AGGCC AGGCC AGGCC AGCT G CAAA AC AA CT GAGG C ACCA AGA ATG  
 TT G CCAG TT G TACT G AAT C AT C AAGT CC AT AT GTT ACCT C AT AAGT CAC CT GT CAC  
 CACT T TAGATAAGAG C ACT GGC ATT GAG AT CT CT ACAG AAT CAGA AG AT GTT CCCT CAG CT CT  
 CAGGT GAA ACT T GCG ATAG AAAA ACCCG AAGAG GTT GGAA AGC ACCC AGAG AGT T GGA ATA AT  
 GAT GAC AT TT GAAAAA ATT T TAGAT ATT AATT CAC AAGT GCA ACAGG CACT T TAGT G A  
 CACCAG CA ACCC AGC AT ATAGAG AAG AT ATT G AAGC CT C TAA AG AT CAC CT AAA AC GA AG CC  
 TT G CT C T A G CAG CAG CAG CAG A AC AT AA ATT AAA AC AT GT T AAGT C CAG TT ATT G CCA  
 GTAGG AC GA AC AAG T AAT AAA ATT GAT GAC AT CG A AACT GT T ATT A AC AT GCT GT G T AAT C  
 TAG AT CT A AACT C T AT G A AT ATT T TAG AT ATT AA AT GT T CC ACCAG AG AT GAG AG AAAA AG  
 CT G CT ACAG T ATT C A ATAC AT T AAAA AT AT GT T GAG AT CA AGG AG AGT CAC AGC CT T ATT A  
 AA AG TT T AT **TAA** ACA AT A AT AAAA ATT TAA AC CT ACT T GAT ATT CC AT A AC AA AG CT G A  
 TT A AG CAA ACT G CATT T T CAC AGG GAG A AT A AT C AT ATT CG T A ATT C AAA AG TT GT T AT  
 AAAA AT ATT T C ATT GT TAG T CAA AT GT G CCA AC AT CTT AT GT G T C AT GT G T T AT G A A C A  
 AT TT C AT AT G C ACT AAAA AC CT A ATT AAAA ATT TT G GT T CAGG AAAA

## **FIGURE 146**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPSGEPGREKNSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTFPTGGFTPEIGKKKTESTPFWSI
KPNNVSIVLHAEPYIENEPEPEPAAKQTEAPRMLPVVTESSSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPEWNNDDILKKILDINSVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAEEHKLKTMYKSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY
```

**Signal peptide:**

amino acids 1-19

## FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCTGCGCCTGAGACAGCTGGCCTG  
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTCACTAGTGTGAGATCAACCCACA  
 GGAATATCC**ATG**GCTTTGTGCTCATTTGGTCTCAGTTCTACGAGCTGGTGTAGGACA  
 GTGGCAAGTCACTGGACCGGGCAAGTTGTCCAGGCCTGGTGGGGAGGACGCCGTGTTCT  
 CCTGCTCCCTCTTCCTGAGACCAGTCAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAG  
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGAAGACTGGGAATCTAACAGATGCCACA  
 GTATCGAGGGAGAACTGAGTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTAACGGC  
 TAAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGTGCTGGTCAGTCCAGATTAC  
 GATGAGGAGGCCACCTGGGAGCTCGGGGTGGCAGCACTGGCTCACTCCTCTCATTTCCAT  
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCAGGCTGGTTCCCCCAGC  
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTGTCTCAGACTCCAGAGCAAATGCA  
 GATGGGTACAGCCTGTATGATGTGGAGATCTCATTATAGTCCAGGAAAATGCTGGGAGCAT  
 ATTGTGTTCCATCCACCTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG  
 AGACGTTTCCAGCCCTCACCTGGCGCTGGCTTCTATTACTCGGGTTACTCTGTGGT  
 GCCCTGTGTGGTGTGTCATGGGATGATAATTGTTCTTCAAATCCAAGGGAAAATCCA  
 GGCAGGAACGGACTGGAGAAGAACGGACAGGAGAAATTGAGAGACGCCGGAAACACG  
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTACCCGAAGCTCTGCCTTGATCTGAAA  
 ACTGTAACCCATAGAAAAGCTCCCAGGGAGGTGCCTCACTCTGAGAAAGAGATTACAAGGAA  
 GAGTGTGGTGGCTCTCAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGAC  
 AAAATGTAGGGTGGTATGTGGAGTGTGTCGGGATGACGTAGACAGGGGAAGAACAAATGTG  
 ACTTTGTCTCCAAACATGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTCAC  
 ATTCAATCCCCATTATTCAGCCTCCCCCCCAGCACCCCTCTACACGAGTAGGGTCTTCC  
 TGGACTATGAGGGTGGGACCATCTCCTCTTCAAACAAATGACCAGTCCCTTATTATACC  
 CTGCTGACATGTCAGTTGAAGGTTGAGACCTATATCCAGCATGCGATGTATGACGA  
 GGAAAAGGGACTCCCATATTCAATGTCCAGTGTCTGGGA**TGA**GACAGAGAACCCCTG  
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCGACAGGTGGC  
 CCCAGCTCCTCTCCGGAGCCTGCGCACAGAGACTCACGCCCACTCTCCTTAGGGAGC  
 TGAGGTTCTCTGCCCTGAGCCCTGAGCAGCGGAGTCAGCAGCTCAGCTCCAGATGAGGGGGAT  
 TGGCCTGACCCCTGTGGGAGTCAGAACCCATGGCTGCCCTGAAGTGGGAGGAATAGACTCA  
 CATTAGGTTAGTTGTGAAAATCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC  
 CAGGCTCCTCATTGCTAGTCAGGGACAGTGATTCCCTGCCCTCACAGGTGAAGAGATTAAAGAGA  
 CAACGAATGTGAATCATGCTGCAAGTTGAGGGCACAGTGTTGCTAATGATGTTTTA  
 TATTATACATTTCCCACCATAAACTCTGTTGCTTATTCCACATTAATTACTTTCTCTA  
 TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTGTGAGGCTCAAAGAATAAGAG  
 GAGGTAGGATTTCACTGATTCTATAAGCCAGCATTACGATACCAAAACCAGGCAAAG  
 AAAACAGAAGAAGAGGAAGGAAAATCACAGGTCCATATCCCTCATTAACACAGACACAAAAAA  
 TTCTAAATAAAATTAAACAAATTAAACTAAACATATTTAAAGATGATATATAACTACT  
 CAGTGTGGTTGTCCCACAAATGCAGAGTTGTTAATATTAAATATCAACCAGTGTAAATT  
 CAGCACATTAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAAA

## **FIGURE 148**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866  
><subunit 1 of 1, 466 aa, 1 stop  
><MW: 52279, pI: 6.16, NX(S/T): 2  
MAFVLILVLSFYELVSGQWQVTGPGKVFQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA  
VVHLYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE  
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPOGQDLSSDSRANADGY  
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGILCGALC  
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWWVGVCRDDVDRGKNNVTLS  
PNNGYWVLRLTTEHYFTFNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLT  
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

## FIGURE 149

CCTTCACAGGACTCTCATTGCTGGTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA  
 GGAAAAGAGTTGTTGGAACCCCTGGGTATCGGCCTCGTCATCTCATATCCCTGATTGTC  
 CTGGCAGTGTGCATTGGACTCACTGTTCATTATGTGAGATATAATCAAAGAACCTACAA  
 TTACTATAGCACATTGTCATTACAACGTACAAACTATATGCTGAGTTGGCAGAGAGGCTT  
 CTAACAATTACAGAAATGAGCCAGAGACTTGAATCAATGGTAAAAATGCATTTATAAA  
 TCTCCATTAAGGAAGAATTGTCAAGTCTCAGGTTATCAAGTTCAAGTCAACAGAACATGG  
 AGTGGTGGCTCATATGCTGTTGATTGTAGATTCACTCTACTGAGGATCCTGAAACTGTAG  
 ATAAAATTGTTCAACTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTA  
 GATCCTCACTCAGTAAAATTAAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
 TTGCTGCGGAACACGAAGAAGTAAAACCTCTAGGTCAGAGTCTCAGGATCGTGGTGGACAG  
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGATGGAGTCATCGCTGT  
 GGAGCAACCTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTACAACATATAA  
 GAACCCCTGCCAGATGGACTGCTTCCTTGGAGTAACAATAAAACCTCGAAAATGAAACGGG  
 GTCTCCGGAGAATAATTGTCATGAAAATACAAACACCCATCACATGACTATGATATTCT  
 CTTGCAGAGCTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTGTCTCCCTGA  
 TGCATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAAA  
 ATGATGGTTACAGTCAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC  
 TGCAATGAACCTCAAGCTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCT  
 AGAAGGAAAAACAGATGCATGCCAGGGTGAECTGGAGGACACTGGTAGTTAGTCAGATGCTA  
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCCAACAAG  
 CCTGGTGTATTAATCTAGAGTTACGGCCTTGCAGGACTGGATTACTCAAAAATGGTATCTA  
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTGGGTGTGGAGGCCATT  
 TTTAGAGATAACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTAATAAAC  
 TGTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGTTCTG  
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTATGTACATAGAGAAATAGATA  
 ATACAATATTACATTACAGCCTGTATTCACTTGTCTCTAGAAGTTGTGAGAATTGAC  
 TTGTTGACATAAATTGTAATGCATATATAACATTGAAAGCACTCCTTCTCAGTTCTC  
 AGCTCCTCTCATTCAGCAAATATCCATTTCAGGTCAGAACAGAGTGAAAGAAAATA  
 TAAGAAGAAAAAAATCCCCTACATTATTGGCACAGAAAAGTATTAGGTGTTTTCTTAGT  
 GGAATATTAGAAATGATCATATTCACTTGTGAGCAAGCTAACAGCAGAACATACCAATC  
 ACTTCATCATTAGGAAGTATGGGAACACTAAGTTAAGGAAGTCCAGAAAGAACAGCAAGATATA  
 TCCTTATTTCATTCACAAACAACTACTATGATAATGTGAAGAAGATTCTGTTTTGTG  
 ACCTATAATAATTACAAACTCATGCAATGTACTTGTCTAAGCAAATTAAAGCAAATAT  
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCCA

## **FIGURE 150**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVNAFYKSPREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELOSSPVPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

**Transmembrane domain:**

amino acids 21-40 (type II)

## **FIGURE 151**

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATAACAACCTGACAGCA  
 CAGCCTGAGATCTGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG  
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGCTCTCCCTGCCTCTGTGGCTCCTGGC  
 CGTGACCTCTTGGTCCCAGAGCTCAGCCCTGGCCCTCAAGACTTGAAGAAGAGGAGG  
 CAGATGAGACTGAGACGGCGTGGCCGCCCTTGGCCGGCTGTCCCCCTGCGACTACGACCACTGC  
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTGGGCCGGCGCCTGCCTGTGCC  
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCATGGAGAAGTGCAGCTTGC  
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCTCTCCCCGGTCTCCACTACTGG  
 CTGCTGCTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCGCTGAACGCTACGGTCCG  
 CAGAGCCGAACTGAAGGGCTGAAGCCAGGGCATTATGTCGTTGCGTAGTGGCCGCTA  
 ACGAGGCCGGGCAAGCCGCGTGCCCAAGGCTGGAGGAGAGGGCCTCGAGGGGCCGACATC  
 CCTGCCTTCGGGCCTTGCAGCCGCCTTGCAGGCCCAACCCCCGCACTCTGGTCCACGC  
 GGCGTCGGGTGGCACGGCCCTGGCCCTGCTAACGCTGTGCCGCCCTGGTGTGGCACTTCT  
 GCCTGCGCGATCGCTGGGCTGCCCGCCGAGCCGCCGAGCCGAGGGCGCT**TGA**  
 AAGGGGCCTGGGGCATCTGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG  
 GGAAAAGAGGAAAACCGCTGCCCTCAGGGAGGGCTGGACGGCGAGCTGGAGCCAGCCCCAG  
 GCTCCAGGGCCACGGCGAGTCATGGTCTCAGGACTGAGCGCTGTTAGGTCCGGTACTT  
 GCGCTTGTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCAATTTTTTTA  
 AGCGGCCAGATAATAATAATGTAACCTTGCAGGTTAAAAAAAAAAAAAAA

## **FIGURE 152**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPNATVRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADI PAFGPCSRL
AVPPNPRTLVHAAGVGTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

## **FIGURE 153**

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCGCGAAGAAGTTC  
CTGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCAGGGCTGGGCACCGGG  
CCCAGCGCCGACGATCGCTGCCGTTGCCCTTGGGAGTAGGATGTGGTAAAGGATGGGC  
TTCTCCCTAACGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCCTGCCTGCT  
CTACGCCCTCAATCTGCTTTGGTTAATGTCCATCAGTGTGGCAGTTCTGCTTGG  
TGAGGGACTACCTAAATAATGTTCTCACTTAAC TGAGAAACGAGGGTAGAGGAAGCAGTC  
ATTTGACTTACTTCCGTGGTCATCCGGTCA TGATTGCTGTTGCTGTTCTTATCAT  
TGTGGGATGTAGGATATTGTGGAACGGTAAAAGAAATCTGTTGCTTGGCATGGTACT  
TTGGAAGTTGCTTGTCAATTCTGTAGAAACTGGCTTGGCGTTGGACATATGAACAG  
GAACTTATGGTCCAGTACAATGGTCAGATATGGTCAC TTGAAAGCCAGGATGACAAATTA  
TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTCAGAGAGAGTTAAGT  
GCTGTGGAGTAGTATATTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGAT  
TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCAAACAGGCCACCAGGAAGATCTCAGTGA  
CCTTATCAAGAGGGTGTGGGAGAAAATGTATTCCCTTTGAGAGGAACCAAACAAC  
AGGTGCTGAGGTTCTGGGAATCTCCATTGGGTGACACAAATCTGCCATGATTCTCACC  
ATTACTCTGCTCTGGCTCTGTATTATGATAGAAGGGAGCCTGGACAGACCAAATGATGTC  
CTTGAAGAATGACAACCTCAGCACCTGTCA TGTCCTCAGTAGAAACTGTTGAAACCAAGCC  
TGTCAAGAATCTTGAACACACATGGCAAACAGCTTAATACACACTTGAGATGGAG  
GAGTTTAAAAAGAAATGTACAGAAGAAAACCACAAACTGTTTATTGGACTTGTGAATT  
TTTGAGTACATACTATGTGTTCAGAAATATGATAGAAATAAAATGTTGCCATAAAATAACA  
CCTAAGCATATACTATTCTATGCTTAAAATGAGGATGGAAAAGTTCATGTCATAAGTCAC  
CACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
CTGTGTATGACTTTACTGAACACAGTTATGTTGAGGCAGCATGGTTGATTAGCATTTC  
CGCATCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGTGATTTACTT  
CTACCAAACATAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA  
ACTTTATTACTCAGCGATCTATTCTGATGCTAAATAATTATATCAGAAAACCTTC  
AATATTGGTACTACCTAAATGTGATTTGCTGGTTACTAAAATATTCTACCACTTAAA  
GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTGGTATATAAGTCTGTGTTAAA  
TCTGTATAATTCACTGATTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA  
ATTGTCCTGTATAGCATCATTATTTAGCCTTCTGTTAATAAAAGCTTACTATTCTGT  
CCTGGCTTATATTACACATATAACTGTTATTAAATACTTAACCACTAATTGAAAATTA  
CCAGTGTGATACATAGGAATCATTATTCAAGATGTTAGTCTGGTCTTAGGAAGTTAAATAA  
GAAAATTGACACATAACTTAGTGATTCAGAAAGGACTTGTATGCTGTTCTCCCAAATG  
AAGACTCTTTGACACTAACACTTTAAAAGCTTATCTTGCCCTCTCCAAACAAAGAA  
GCAATAGTCTCCAAGTCATATAAATTCTACAGAAAATAGTGTCTTTCTCCAGAAAAT  
GCTTGTGAGAATCATTAAAACATGTGACAATTAGAGATTCTTGTGTTATTCACTGATTA  
ATATACTGTGGCAAATTACACAGATTATAAATTGTTACAAGAGTATAGTATATTATT  
GAAATGGGAAAAGTGCATTACTGTATTGTTATTCTCAGAATATGGAA  
AGAAAATTAAATGTGTCATATAAATTCTAGAGGTTAA

## **FIGURE 154**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPV
VHPV рIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMNTNYGLPRYRWLTHAWNFFQREFKCCGVYFTDWLEMTEMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPГTDQMMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

## FIGURE 155

GAGAGAGGCAGCAGCTGCTAGCGGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCC  
 TGCACCTGGGCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA  
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTGGGTGACAATCTCAGCTCCAGGCTACAGGGAG  
 ACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC  
 CTCGATGTCAAACCCCTGCGCAAACCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGAT  
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGCCTCATCAAGG  
 TGATTCTGGATAAATACTACTTCCTCTGCAGCCTCTCCACTTCATCCGAGGAAGCAG  
 CTGTGTGACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT  
 CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG  
 ACTCGGCCACAGGAACTGGTCTCTGCCTGTTGACAACCTCACAGAAGCTCTCGCTGAG  
 ACAGCCTGTAGGCAGATGGCTACAGCAGAGCTGTGGAGATTGCCAGACCAGGATCTGGA  
 TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTCGATCGGAACACTCAAGTGGCCCTGTC  
 TCTCAGGCTCCCTGGCTCCCTGCACTGTCTGCCTGTGGGAAGAGCCTGAAGACCCCCCGT  
 GTGGTGGGTGGGGAGGAGGCCTCTGGATTCTTGGCCTGGCAGGTGAGCATCCAGTACGA  
 CAAACAGCACGTCTGTGGAGGGAGCATTGGACCCCCACTGGTCCTCACGGCAGCCCAGT  
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGC  
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCATGTACCCAA  
 AGACAATGACATGCCCTCATGAAGCTGCAGTCCCACTCACTTCTCAGGCACAGTCAGGC  
 CCATCTGTCTGCCCTTTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATTGGA  
 TGGGGCTTACGAAGCAGAATGGAGGGAAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA  
 GGTCAATTGACAGCACCGTCAATGCAGACGATGCGTACCGAGGGAAAGTCACCGAGAAGA  
 TGATGTGTGCAGGCATCCCGAAGGGGTGTGGACACCTGCCAGGGTACAGTGGTGGGCC  
 CTGATGTACCAATCTGACCAGTGGCATGTGGGGCATCGTTAGCTGGGCTATGGCTGC  
 GGGCCCGAGCACCCAGGAGTACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG  
 TCTGGAAGGCTGAGCTG**TAAT**GCTGCTGCCCTTGCACTGCTGGAGCCGCTCCTCCTG  
 CCCTGCCACCTGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTGGTACACCC  
 CTCTGCCACAGCCTCAGCATTCTGGAGCAGCAAAGGGCTCAATTCTGTAAGAGACCC  
 TCGCAGCCCAGAGCGCCCAGAGGAAGTCAGCAGCCCTAGCTGCCACACTGGTGCTCCC  
 AGCATCCCAGGGAGAGACACAGCCCAGTGAACAAGGTCTCAGGGTATTGCTAAGCCAAGAA  
 GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTGAAAAGCCCAGATCACTGTGGG  
 CTGGAGAGGAGAAGGAAAGGGTCTGCCAGCCCTGTCCGTCTCACCCATCCCCAAGCCTA  
 CTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT  
 ACCTACTGTTGTCATTGTTATTACAGCTATGCCACTATTATAAGAGCTGTAAACATCT  
 CTGGCAAAAAAAA

## **FIGURE 156**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVVLIKVILDKYYF
LCGQPLHFI PRKQLCDGELDCPLGEDEEHCVKSFP EGPAVAVRLSKDRSTLQV LDSATGNWF
SACFDNFTEAL AETACRQMGYSRAVEIGPDQ DLDV VEITENSQELRMRNSSGPCLSGSLVSL
HCLACGKSLKT PRVVGEEASVDSWPWQVSIQYDKQHVC GGSILD PHWL TAAHCFRKHTDV
FNWKVRAGSDKLGSF PSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGT VRPICLPFFD
EEILT PATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDT CQGD SGGPLMYQSDQWHVVGIVSWG YGC GGPSTPGVYTKV SAYLNWIY NVWKAEL
```

**Transmembrane domain:**

amino acids 32-53 (typeII)

## FIGURE 157

GGGCTGAGGCAGTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGCATCCCCAGGCTCCAG  
 AGCTCCCTGGTGACAGTCTGTGGCTGAGC**ATG**GCCCTCCAGCCCTGGCCTGGACCCCTGGAGCCTCCTGGCC  
 TTTCCCTTCCAAC TGCTCAGCTGCTGCCAGCAGCAGCGGGGGAGGCAGGGCAGGGGCCATGCCA  
 GGGTCAGATACTATGCAGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTGACA  
 CTCTGCTCCTGAGTGGTATGGAAATACTCTACGTGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGG  
 ATCCAGGGTCCCCAGGCTAAAGAACATGATAACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTA  
 AGAAGAACAGCAATGAGACACAGTGTTCACCTCATCGCTGGTTCTACAATGTCACCCATCTCTACA  
 CCTGGGGCACCTCGCCTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATCCTACCTGTTGCCATCTCGG  
 AGGACAAGGTATGGAGGGAAAGGCCAAAGCCCCTTGACCCGCTCACAAGCATAACGGCTGTCTGGTGGATG  
 GGATGCTCTATTCTGGTACTATGAACAACTTCTGGCAGTGAGCCATCCTGATGCGCACACTGGATCCCAGC  
 CTGTCCTCAAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCTCCTTGACTGAGCCATCCCTCGACCC  
 AGGTGCTACTTCTTCGAGGAGACAGCCAGCGAGTTGACTTCTTGAGAGGGCTCCACACATCGGGGTGG  
 CTAGAGTCTGCAAGAACATGACGTGGCGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTCCTGAAGGCCAGC  
 TGCTCTGCACCCAGCCGGGGCAGTGCCTTCAACGTCATCCGCCACGCCGCTGCTCCCCGCCGATTCTCCA  
 CAGCTCCCCACATCTACCGAGTCTCACCTCCAGTGGCAGGTTGGCGGGACCAGGAGCTGCGGTTGTGCCT  
 TCTCTCTTGGACATTGAACGTCTTAAGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  
 CTTATAGGGCCCTGAGACCAACCCCCGCCAGCAGTTGCTCAGTGGCCCTCCTGATAAGGCCCTGACCT  
 TCATGAAGGACCATTCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGGTAAATCTGGCGTGGAGTATA  
 CACGGCTGCACTGGAGACAGCCAGGGCTTGTGGCACAGCCATCTGTCACTGTACCTGGAACCAACACAG  
 GGTGCTCCACAAGGCTGTTAAGTGGGACAGCAGTGCTCATCTGGTGGAAAGAGATTGAGCTGTTCCCTGACC  
 CTGAACCTGTCGAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGGTGTAGGCTCTCAGGAGGTGTCTGGA  
 GGGTCCCCGAGCCAACGTAGTGTCTATGAGAGCTGTGTGACTGTGTCCTTGGCCGGACCCCCACTGTGCCT  
 GGGACCTGAGTCCCGAACCTGTTGCCCTGTCTGCCCTAACCTGAACCTGAACTCCTGGAAGCAGGACATGGAGCGGG  
 GGAACCCAGAGTGGCATGTGCCAGTGGCCCTGAGCAGGAGCCTCGGCCTCAGAGGCCCGCAAATCATTA  
 AAGAAGTCCTGGCTGTCCCCACTCCATCTGGAGCTCCCTGCCCTGAGCAGCTGGCTTATTATTATT  
 GGAGTCATGGCCAGCAGCAGTCCAGAAGCCTTCCACTGTCTACAATGGCTCCCTTGCTGATAGTGCAGG  
 ATGGAGTTGGGGCTCTACCAAGTGTGGCAACTGAGAATGGCTTTCATACCTGTGATCTCTACTGGGTGG  
 ACAGCCAGGACCAGACCCCTGGCCTGGATCCTGAACCTGGCAGGACATGGCAGGAGCTGAGGTGGCTGA  
 CCAGGGCTGAGACCCCTGCCAGTGGCCCTGGCTGCCAGCAGTCCACTGGCCCTACTTGTCACTGTCACTGTCT  
 TTGCTTAGTGCTTCAAGGAGCCCTCATCATCTCGTGGCTCCCTGAGAGACACTCCGGCTGGGCAAGG  
 TTCAGGGCTGTGAGACCCCTGCCAGTGGCAGGACCTGGCCATGCTGGCTGGCGGGCCAAGCACAGCCCTGACTAGG  
 AATGCAGGACCTCTGCCAGTGTGGACGCTGACAACAACGCTAGGCACTGAGGTAGCT**TAA**ACTCTAGGCA  
 CAGGCCGGGCTGCCAGCAGGACCTGGCCATGCTGGCTGGCGGGCCAAGCACAGCCCTGACTAGGATGACAG  
 CAGCACAAAAGACCACCTTCTCCCTGAGAGGGCTGTGCTACTCTGCATCACTGATGACACTCAGCAGGGT  
 ATGCACAGCAGTCTGCCCTCATGGACTCCCTCTACCAAGCAGCAGTGGAGAGGATCCTCAGTCTGGCATTCCAGGGACCC  
 CCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGAGCTGCTACTCTGCATCAACAGGGTGGGGCTAC  
 CAGAAACACAGTGTTCAGAGAGACCCCTAAAAAACCTGCCCTGGCTCCAGGACCCCTATGGTAATGAACACCAACATC  
 TAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCCTTGGACACCAACACTCC  
 TCTCCAGGGTATGCCAGGGATCTGCTCCCTCCTGCTTACCAAGTGTGCAACCGCTGACTCCCAGGAAGTC  
 TTTGCTGAAGTGTGACCACCTTCTTGCTTCACTCCTTACCCCTAGCTGACCCCTCACCTCTCCCCCTCC  
 CAGGGTAATCTGAGCCTTCTCACTCCTTACCCCTAGCTGACCCCTCACCTCTCCCCCTCC  
 TTTGGATTCAAGAAACTGCTTGTCAGAGACTGTTATTAAAAATAAGGCTAAAAAA

## FIGURE 158

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLLQLLLPTTAGGGQGPMPPRVRYYAGDERRALSFFHQKGLQ
DFDTLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVFVFF
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFIMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLV
YLGTTTGSLLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPEPRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAQVNSILELPCPHLSALASYYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVVKVPLTRVSGGAALAAQSYWP
HFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVEDADNNCLGTEVA

```

**Signal peptide:**

amino acids 1-30

**Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704

## FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG  
 TGAGC**ATG**GCTGGGCAGCGAGTCTTCTAGTGGCTTCTCCCTGGGTCCTGCTC  
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA  
 CCGGGTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCATGCTAACCAACAAAAGAG  
 GTCCTTTATGCCAGATTTAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCTTGCA  
 CCTGAAGATCATCAAAGAGAATTAAAAGAGTTGATTTCTGAAACTTGGCAGTGCAGTC  
 TGGCAGAGGAAAATTGAAAACCTATAAATGTTCTAGAATACTTGGCAGTGCAGTC  
 ATTTTTAAATAGAAAGGATATCATGGATTCCCTAAAGAATGAGAACTTCGACATGGTGATA  
 GTTGAACACTTTGACTACTGTCCTTCCTGATTGCTGAGAAGCTGGGAAGCCATTGTGGC  
 CATTCTTCACTTCATTGGCTCTTGGATTGGCTACCAATCCCCTGTCTATGTT  
 CAGTATTCCGTTCTGACTGATCACATGGACTTCTGGGCGAGTGAAGAATTTCTG  
 ATGTTCTTCTGAGTTCTGAGGAGGCAACAGCACATGCAGTCTACATTGACAACACCATCAA  
 GGAACATTCACAGAAGGCTAGGCCAGTTGTCTCATCTTCACTGAAAGCAGAGTTGT  
 GGTCATTAACCTGACTTGCCTTGATTTGCTGACCTCTGCTTCCAAACACTGTTAT  
 GTTGGAGGCTTGATGGAAAACCTATAAACCAGTACCAAGACTGGAGAACTTCATTGC  
 CAAGTTGGGACTCTGGTTTGTCCCTGTGACCTTGGCTCATGGTAACACCTGTCAGA  
 ATCCGGAAATCTCAAGGAGATGAACAAATGCCCTTGCTCACCTACCCCAAGGGGTGATATGG  
 AAGTGTCACTGTTCTCATGGCCAAAGATGTCACCTGGCTGCAAATGTGAAATGTGGA  
 CTGGCTTCTCAGAGTGACCTCTGGCTCACCAAGCATCCGTCTGTTGTCACCCACGGCG  
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGATCCCTCTTT  
 GGAGACCGAGCTGAAAACATGGTCCAGTAGAAGCCAAAAGTTGGTGTCTATTCAAGTT  
 AAAGAAGCTCAAGGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
 ACAAGTCCGGCAGTGGCTGCCAGTGTCTGCGCTCCCACCGCTCAGCCCCACACAG  
 CGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCAGCACCTCAAGCCCTA  
 TGTCTTCAGCAGCCCTGGCATGAGCAGTACCTGTCACGTTTGTGTTCTGCTGGG  
 TCACTCTGGGACTCTATGGCTTGTTGGAGCTGCTGGCATGGCTGTCTGGTGGCTGCGT  
 GGGGCCAGAAAGGTGAAGGAGACA**TAA**GGCCAGGTGCAGCCTTGGGGGCTGTTGGTGG  
 GCGATGTCACCATTCTAGGGAGCTCCCCTAGTTCTGGCAGCCCCATTCTCTAGTCCTC  
 TAGTTATCTCCTGTTCTGAAGAACAGGAAAATGCCAAAATCATCCTTCACTTGC  
 TAATTTGCTACAAATTCTACCTTACTAGCTCTGCTGCTAGCAGAAATCTTCACTTGC  
 CTTGTCCTCTTGTGCTCAGCAAGGGCTATGCTGTGATTCTGTCTGAGTGACTTG  
 GACCACTGACCTCAGATTCCAGCCTAAACACCTTCTCATGCGCCTCTCCGAA  
 TCACACCCCTGACTCTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCACTCC  
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTGCAATATTCTTCAGTTCTGTT  
 TGTTCTCCACATATTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCA  
 CGGACACAGGCTCACAGGTCTCCACATTGGGCTCCATGGTGCCTCTGGTCCCACAGT  
 GAGCTCCTTGGCTGAGCAGGCATGGAGACTGTAGGTTCCAGATTTCTGAAAAA  
 ATAAAGTTACA  
 GCGTTATCTCTCCCCAACCTCACTAA

## **FIGURE 160**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169  
><subunit 1 of 1, 523 aa, 1 stop  
><MW: 59581, pI: 8.68, NX(S/T): 1  
MAGQRVLLLGVFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTMLNHKRGP  
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF  
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPV  
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLIKELWF  
INSDFAFDFARPLLPNTVYVGGLMEKPIKPVHQDLENFIAKFGDSGFVLVTLGSMVNTCQNP  
EIFKEMNNAFAHLPQGVIWKCQCSHWPKDVKLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ  
NSIMEAIQHGVPVMVGIPPLFGDQOPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK  
SAAVAASVILRSHPLSPTQRILVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDVFVFLGLT  
LGTLWLCGKLLGMAVWWLRGARKVKET

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

## FIGURE 161

GGGCTGTTGATTGTTGGGGATTTGAAGAGAGGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTACACACACATACCATGTT  
 CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGCTCCATCCAGCAGGGCTACCCCTGAAGCTCT  
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTCATCCCTTCTCTCCCAAAGGCCA  
 ACTGCTGTCAGTGCATGCTGCAAGGAGGAGGAACTGCAGTGACAGCAGGAGTAAGAGT  
 GGGAGGCAGGACAGAGCTGGACACAGGTATGGAGAGGGGTTAGCGAGCCTAGAGAGGGC  
 AGACTATCAGGGTGCCGGCGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGCAGA  
 AGACCGGGCACTTGTGGGTGCAGAGCCCCTCAGCC**ATG**TTGGAGCCAAGCCACACTGGC  
 TACCAGGTCCCTACACAGTCCCGGCTGCCCTGGTTCTGGTGCCTGGCCCTGGGGCC  
 GGGTGGGCCAGGAGGGTCAGAGCCGCTCTGCTGGAGGGGAGTGCCTGGTGGTGTGA  
 GCCTGGCCGAGCTGCTGCAGGGGGCCGGGGAGCAGCCCTGGAGAGGCACCCCTGGC  
 GAGTGGCATTGCTGCGGTCCGAAGCCACCATGAGCCAGCAGGGAAACCGGCAATGGC  
 ACCAGTGGGCCATCTACTTCGACCAAGGTCTGGTGAACGAGGGCGTGGCTTGACCGGGC  
 CTTGGCTCCTCGTAGCCCTGTCCGGGTGTCTACAGCTCCGGTCCATGTGGTGAAGG  
 TGTACAACCGCAAACGTCCAGGTGAGCCTGATGCTGAACACGTGGCTGTCACTCAGCC  
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACAGCTCTGTGCTACTGCCCTTGG  
 CCCTGGGGACCGAGTGTCTGCGCCTGCGTCGGGGAAATCTACTGGTGGTGGAAATACT  
 CAAGTTCTCTGGCTTCCTCATCTTCCCTCT**TGA**GGACCAAGTCTTCAAGCACAAGAAT  
 CCAGCCCCTGACAACCTTCTCTGCCCTCTTGCCTGGGAAACAGCAGAGGCAGGGAGAG  
 ACTCCCTCTGGCTCTATCCACCTCTTGATGGACCTGTGCCAAACACCCAGTTAA  
 GAGAAGAGTAGAGCTGGCATCTCCAGACCAGGCCTTCCACCCACCCACCCAGTTAC  
 CTCCAGCCACCTGCTGCATCTGTTCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTGGCA  
 AGAAGGAAGATCTGCACTACTTGCAGGCTCTGCTCTCCGGTCCCCCACCCAGCTTCC  
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCACAGGGAGCCAG  
 ATGGACAAGCCTCAGCGTACCCCTGCAGGCTTCTCCTGTGAGGAAAGCCAGCATCAGGATC  
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGCTAGGGTGGGAGGCTCAGCCAC  
 AGGCAGAAGGGTGGGAAGGGCTGGAGTCTGGCTGGTGGAGGAAGGAGGGTGTATTG  
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGGTAGCAATCCT  
 GGCTGTCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTAACCTCCCCACCTGAGATTAG  
 GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
 ACCATGGAAAACATCGATAACCACATGCATCCTCTGCTGGCCACCTCCTGAAACTGCTCCAC  
 CTTGAAGTTGAACCTTACTGCTCCACACTCTGACTGCTGCCTCCTCCTCCAGCTCTC  
 TCACTGAGTTATCTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCTGAT  
 CTGTGCTGTCTTATTCTCCTCTTAGGCTTCTATTACCTGGGATTCCATGATTCAATTCTT  
 CAGACCCTCTGCCAGTATGCTAAACCCCTCTCTCTTCTTATCCCGCTGCTCCATT  
 GGCCAGCCTGGATGAATCTATCAATAAAACAACAGAGAATGGTGGTCAGTGAGACACTAT  
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTGGATCGGGTGTACAGGTACAAGTAGGTA  
 TGGTGCAGAGGAAAATAATCAAACGTATACTAAAATTAAAAA

## **FIGURE 162**

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGR
AAAGGPGGA
ALGEAPPGRVAFAAVRSHHEPAGETGNGTSGAIYFDQVLVNEGGFDRASGSFVAP
VRGVY
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFA
NDPDVTREAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

**Signal peptide:**

amino acids 1-32

## FIGURE 163

GCTGTTCTCGGCCACCACTGGCCGCCGGCGCAGCTCCAGGTGTCCTAGCCGCCAGC  
 CTCGACGCCGTCCGGGACCCCTGTGCTCTGCGCAAGCCCTGGCCCCGGGGCCGGGCAT  
 GGGCCAGGGCGCGGGGTGAAGCGGCTCCCGCGGGCGGTGACTGGCAGGCTCAGGCC**AT**  
**GA**AGACCCCTCATAGCCGCCTACTCCGGGTCTGCGCGCGAGCGTCAGGCCGAGGCTGACC  
 GGAGCCAGCGCTCTCACGGAGGACCTGCGCTGCGCGAGGGTCTGGAGATGGGCACT  
 GGATCCAGCATCCTCTCCGCCCTCCAGGACCTTCTGTCACCTGGCTCAATAGGTCAA  
 GGTGGAAAAGCAGCTACAGGTATCTCAGTGCTCCAGTGGCTCTGCTCCTGTACTGG  
 GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTCATCGCTGTG  
 CTCTACTTCACTGGCTGGTGTGTTGACTGGAACACACCAAGAAAGGTGGCAGGAGGTACA  
 GTGGGTCCGAAACTGGCTGTTGCGCTACTTCGAGACTACTTCCCATCCAGCTGGTGA  
 AGACACACAAACCTGCTGACCACCAGGAACATATCTTGGATACCACCCCCATGGTATCATG  
 GGCCTGGGTGCCTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTCCCAGG  
 CATA CGGCCTTACCTGGCTACACTGGCAGGCAACTCCGAATGCCGTGTTGAGGGAGTACC  
 TGATGTCTGGAGGTATCTGCCCTGTCAGCCGGACACCATA GACTATTGCTTCAAAGAAT  
 GGGAGTGGCAATGCTATCATCATCGTGGTCGGGGTGCGGCTGAGTCTTGAGCTCCATGCC  
 TGGCAAGAATGCAGTCACCCCTGCGGAACCGCAAGGGCTTGTGAAACTGCCCTGCGTCATG  
 GAGCTGACCTGGTCCCCTACTCCTTGGAGAGAATGAAGTGACAAGCAGGTGATCTC  
 GAGGAGGGCTCCTGGGCCGATGGTCCAGAAGAAGTCCAGAAATACATTGGTTGCC  
 ATGCATCTCCATGGCGAGGCCTTCTCCTCCGACACCTGGGGCTGGTGCCTACTCCA  
 AGCCCATCACCACGTGGAGAGGCCATCACCATCCCCAAGCTGGAGCACCCAAACCCAG  
 CAAGACATCGACCTGTACCAACCCATGTACATGGAGGCCCTGGTAAGCTCTCGACAAGCA  
 CAAGACCAAGTCGGCCTCCGGAGACTGAGGTCTGGAGGTGAAC**TGA**GCCAGCCTCGGG  
 GCCAATTCCCTGGAGGAACCAGCTGCAAATCACTTTTGCTCTGAAATTGGAAAGTGTCA  
 TGGGTGTCTGGTTATTTAAAGAAATTATAACAATTGCTAAACCAAAAAAAA  
 AAAAAAAA  
 AAAAAAAA

## **FIGURE 164**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pi: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAVLYFTWLVFDWNTPKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKFP
GIRPYLATLAGNFRMPVLREYLMGGICPVSRTDIDYLLSKNGSGNAIIVVGGAAESLSSM
PGKNAVTLRNRKGKVKLALRHGADLVPYSGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTGFGLPETEVLEVN
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

## FIGURE 165

GGGCGGGGGATGGGGGCCGGGGCGGGCGCCGACTCGCTGAGGCCCGACGCAGGCCGGCGGGCCA  
 GGGCGAGGAGCGCGGCCAGAGCGGGCGCGAGGCAGCAGCCGGACGCCCGCGACGAGCAGGTGGCG  
 GCGCTGCAGGCTTGTCCAGCGGAAGCCCTGAGGGCAGCTGTTCCACTGGCTCTGCTGACCTTGTGCCTGG  
 CGGCTGTCCTCAGCGAGGGCGTGCACCCGCTCCTGAGCAGCGCAATGGGCCTGCTGGCCTTCTGAAGACCCA  
 GTTCGTGCTGCACCTGCTGGTGGCTTGTCTCGTGGTGGTCTGGTCATCAACTTCGTCCAGCTGTGCAC  
 GCTGGCGCTGGCGGTCAAGCAAGCAGCTTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA  
 ACTGGTCATGCTGCTGGAGTGGTGGCTTGACGGAGTGTACACTGTTACGGACCAGGCCAGGTAGAGCGCTT  
 TGGGAAGGAGCACGCAGTCATCATCCTCAACCACAACTTCGAGATCGACTTCCCTGTGGTGGACCATGTGTGA  
 GCGCTCGGAGTGTGGAGCTCCAAGGTCTCGCTAAGAAGGAGTGTCTACGTGCCCTCATCGGCTGGAC  
 GTGGTACTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG  
 GCGCCTGTCGACTACCCGAGTACATGTGGTTCTCCTGACTGCCAGGGACCGCGCTCACGGAGACCAAGCA  
 CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCCCTGCTCTCAAGTACCAACCTGCTGCCGCGGACCAAGGG  
 CTTCACCAACCGCAGTCAGTGCCTCCGGGGACAGTCGAGCTGTCTATGATGTAACCTGAACCTCAGAGGAAA  
 CAAGAACCGTCCCTGCTGGGATCCTCTACGGGAAGAAGTACGAGCGGACATGTGCGTGGAGGAGATTCCCTCT  
 GGAAGACATCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTACAAACTGTACCGAGGAGACCGCGCTCCA  
 GGAGATATATAATCAGAAGGGCATGTTCCAGGGAGCAGTTAACGCTGCCGGAGGCCGTGGACCCCTCTGAA  
 CTTCTGTCCTGGGCCACCATTCTCCTGTCCTCCCTCTCAGTTTGTCTTGGCGTCTTGCCAGCGGATCACC  
 TCTCCTGATCCTGACTTCTTGGGTTGTGGAGCAGCTTCCCTGGAGTTCGAGACTGATAGGAGAACGCT  
 TGAACCTGGAGGTGGAGATTGCAGTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT  
 CAGCTCAAAAAAAAAACAAAAACCCAGAAATTCTGGAGTTGAACGCTGAGTTACTGACATGAAAA  
 ATTCACTAGAGGCTGAACAGCAGATTGAGCAGGCAGAAAAACAGCAAGCTGAAGATGGTACCTGAGATT  
 TTTCAGGCTAATGAAAAAGAATGAAGGAAATTAAACAGCCTCAGAGACCCATGGCACCCTCACACAAATCAA  
 CATATGCATGATGAGAGTCCCAGAAGGAGAGGAGAAAGGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA  
 GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTCAT  
 AATCAAAGTGTCAAATGACAAAGAATCTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTCAAAGGATCTTG  
 ATCAGATTAACAGCTCATTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA  
 AACCTCAACTGTAATTATTGGACTTTGAGTCTTAGATGGCCTGACCTCTTGTCTTCAGGGACAGTTTCA  
 ATTAATCCCTAATAACAATTAGTCAGCTTCCCTGACCTGTAGGAAGGCTGTCTTAGGCCGGCACAGTGGC  
 TTACACCTGTAATCCCAGCACTTGGGAGGCCAGACGGGATGATCTTGGGATCAGGCTGATCTCAAACCTCCT  
 GAGTTCAGGTGATCTGCCGCCTCAGCCTCCAAAGTGTGATTGCAGGCGTGAGCCACTGCCCTGGCGGA  
 ATTTCTTTAAAGGCTGAATGATGGGGCCAGGCACGATGGCTCACGCCGTGATCCAAGTAGCTGGATTGTA  
 AACATGCACCAACATGCCCTGGCTAATTTGTATTTAGTAGAGACGTGTTAGCCAGGCTGGCTCGATCTCCT  
 GACCTCAAGTGACCACTGCCCTCAGCCTCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTCCTGGCCTTGA  
 GCATCTTGTGATGTGTTATTGCCATTGTATATCTCTATCTTGGGAAATGTCTGTTCAAGTCCTTGC  
 CCTTTTAAATTTTATTATTATTATTGAGACAGGGCTTGTGTTCTGTTGCCAGGCTGGAGTA  
 CAGTGGCACAGTCTGGCTCACTGCAGCCTGCCACCTGGCTGAGTGTACTCCACCTCAGCCTCCCTGT  
 AGCTGTATTTGTATTTGTAGCTGTAGTTGTATTTGTGGAGACAGCATTACCATGA  
 TGCCCAGGCTGGCTTGAACCTCTGAGCTCAAGTGTACTGCTGCCCTCAGCCTCCAAAGTGTGGGATTACAGA  
 CATGAGCCACTGCACCTGGCAAACCTCCAAATCAACACACACACACACACACACACACACACACACACACAC  
 GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTGGCATGAGAAGTCGAGGCTG  
 CAGTGAAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAAACAGAGTGAAGACCCTGTCT

## **FIGURE 166**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFFVVSGLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFIEDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLYHLLPRTKGFTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFSFVLGVFASGSPLILTFILGFVGAASFGVRLIGESLEPGRWRLQ
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169

## **FIGURE 167**

GATATTCTTATTAAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGGCA  
GCCACCAGGCATATTCATCTTGTGTGTTTCTTTGCTTAGCACTGGGGCACTTCTT  
GCTTATTCTTGGTAGGAAAGGGGCTCAGTTGTCTGTGGGGTTGGCAGGCAGGCCG  
GCTTACGCCTGATAACGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTATACAAATGGG  
GATAGCTGGGTCTGAGACCTGCTCCTCAGTAAAATTCTGGATCTGCCTATACCTTCTT  
TTCTCTAACCTGGCATACCCCTGCTTAAAGCCTCTCAGGGCTCTCTGTTCTTAGGATCAA  
AGTATTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCTGCCAGCTCATTGT  
ACATGTGGTGTCTTGTGTTCTG**TAA**TGTGGTATGCCATGGGTCTTGCACAAGCCT  
TTCCTCTTGGCTGGACACTGTTCCCTGCCCTCCACTCTTCTACTTAATATGTAGTC  
ATCCTGCAGATTCAATTCTAACATCATTCTCAGGGATCCTGGCCTGACAGAATCTCAT  
CTTGTAAATGCTCTCATAGACCACCTGTTCCCTTGCAGCAGTGCCTACTCAGTTGTA  
TCTTATGTGCGTTGGTTGTATGGGTGTGCTGTTCCCCAGAATGCCAGCTTGAGC  
TGCCTGAGGGTCAAGGGCATTGCTGTGCCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT  
CATGTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA  
GATGGTGTAGGGCCAGCATTGTAATTACACACGTTGACTGTGCTGTGAATTATCTGGGA  
TGCAGGTCTGATTCACTAGGCCAGGTTGGCATCTCTAACAAACTCCCACGTGATGCTGA  
TGCTGGCCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGCATGGTGGC  
TCACACCTATGATCCCAGCACTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
TCAAGACTAGCCTGGCCAACATGGTGGAACCCATCTGTACTAAAATACACAAATTAGCTG  
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTGGGAGGCTGAAGCAAGAGAATCGCTTGA  
AACCTGGGAGGGGGAGGTTGCAGTGAGCCAGATCAGGCCACTGTATTCCAACCAGGGTGAC  
AGAGTGGAGACTCTATGTCCAAAAAAAAAAAAAA

## **FIGURE 168**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHSLQCPGAATRHIHLCVCFSFALALGHFLLISLVGKGLSLSGVGGRQAGLRLIRPWVRR
EGKINFYTNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

## **FIGURE 169**

GGCTGGACTGGAACCTCCTGGTCCAAGTGATCCACCCGCCTCAGCCTCCAAAGGTGCTGTGA  
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTCAGCAACTAAAAAAGCCAC  
AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGCTAGTGCTCCTACTCCTACCTAC  
ATTAAAATCTGTTTTGTTCTCTTGTAACTAGCCTTACCTTCTAACACAGAGGATCTGT  
CACTGTGGCTCTGGCCCAAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCAC  
ACCGTCCCCTCGAAGCCGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
ACCAACTGTCTCACGTCTGGAGGCAGTGACTCGGGCAGTAGCTGAGGTAGCTGAGCCTTTGGTA  
GCTGCGGCTTCAGGTGGCCTTGCCTGGCGTAGAAGGGATTGAAGAGGAAAGCCGAAGATT  
CATAGGCGATGGCTCCACTGCCAGGCATCAGCCTGCTGTAGTCATCACTGCCCTGGGG  
CCAGGACGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCGCCAT  
CTAACCTTTCATGTCCTGCACATCACCTGATCCATGGCTAATCTGAACACTGTCCCAAGG  
AACCCAGAGCTGAGTGAGCTGAGCTGAGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
TATGTGACAGGACTTGCATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA  
GGGAAGGAACTTGTGCCAAATTATGGGTCAAGAAAGATGGAGGTGTTGGTTATCACAAGGC  
ATCGAGTCTCCTGCATTCACTGGACATGTGGGGAAAGGGCTGCCATGGCGCATGACACACT  
CGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGATCCACGTACCAGCTGCTG  
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAATCTGCGATCACCAG  
CCAGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCCTCCTCCCTC  
TGAGAGGCCCTCTATGTCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGCTAATG  
GCTCAGTGTGGCCAGGAGGTCAAGCAAGGCCTGAGAGCTGATCAGAAGGGCTGCTGTGCG  
AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT  
CAATTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTGTATTGAATTGAAACCCCAA  
TCCAAACCTAAGAACCAAGGTGCATTAAGAATCAGTTATTGCCGGGTGTTGGCCTGTAATG  
CCAACATTTGGGAGGCCAGGGCTAGATCACCTGAGGTCAAGACGCCAGGAGCTGCTGTGCG  
GCCAACATGGTGAACCCCTGTCTACTAAAAATACAAAAAAACTAGCCAGGCATGGTGGT  
GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTGAAACCTGGGAGGT  
GAAGGAGGCTGAGACAGGAGAATCACTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
AAAAATAAAAAAGAATTATGGTTATTTGTAA

## **FIGURE 170**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRD
```

**Signal peptide:**

amino acids 1-15

**FIGURE 171**

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCAGTC  
CCGCCGCCTCCTGCCCGCGCCATGACCCAGCCGGTGCCCGGCTCTCCGTGCCCGCGCCT  
GCCCTGGGCTCAGCCGACTGGCGCCGCCTCGCCACTGGCCTCTTCCCTGGGAGGC  
GCCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCG  
CAGTATCTTCTGAGCCGCTCCATGCAGGGAGCACCCGGCGCTGCGAAGCCTGAGG  
CCTGGAGCAGCCGAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTTGGCAACC  
TGGCGGGCTCATCCAGGCCAAGAAGGGCGCTGGACCTGGCACCTCACGGCTACTCC  
CTGGCCCTGGCCCTGGCGCTGCCCGGGACGGCGCGTGGTACCTGCGAGGTGGAC  
GCCCGGAGCTGGACGGCCCTGTGGAGGCAGGCCGAGGCCGAGCAC  
GGCTGAAGCCCGCCTGGAGACCCCTGGACGAGCTGCTGGCGGGCGAGGCCGG  
GACGTGGCGTGGATGCGACAAGGAGAACTGCTCCGCCTACTACGAGCG  
GCTGCTGCGACCCGGAGGCATCCTGCCGTCCAGAGTCCTGTGGCG  
AACCTCCGAAAGGGGACGTGGCGCCAGTGTGCGAACCTAA  
GACGTAGGGTCTACATCAGCCTCCTGCCCTGGCGATGGACTCAC  
CTGGCCTCAAGATC  
TAGGGCTGGCCCTAGTGAGTGGCTCGAGGGAGGGTGCCTGG  
CCTGAGTTAAATTGAAAAGTGGGCTGGACACAAAAA  
AAAAA

## **FIGURE 172**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGAAAFATGLFLGRRCPWGRGRREQCLLPPEDSRLWQYLLSRS
MREHPALRSLRLTLEQPQGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRLKPALETLDDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRGPGILAVLRLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 8-30, 109-130

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 238-246

**N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

**Amidation sites.**

amino acids 31-34, 39-42

## FIGURE 173

EQUUS • 1999

CCGCCGCCGCAGCCGCTACGCCGCTGCAGCCGCTTCCGGCCTGGGCCTCTGCCGTCA  
 GCATGCCACACGCCCTCAAGCCCAGGGACTTGGTGTTCGCTAAGATGAAGGGCTACCCCTCAC  
 TGGCCTGCCAGGATCGACGACATCGGGATGGGCCGTGAAGCCCCCACCACAAAGTACCC  
 CATCTTTCTTGGCACACACGAAACAGCCTCCTGGACCCAAGGACCTTCCCTACG  
 ACAAAATGTAAAGACAAGTACGGGAAGGCCAACAAAGAGGAAAGGCTTCAATGAAGGGCTGTGG  
 GAGATCCAGAACACCCCCACGCCAGCTACAGGCCCTCCGCCAGTGAGCTCCTCCGACAG  
 CGAGGCCCCCGAGGCCAACCCCGCCACGGCAGTGACGCTGACGAGGACATGAGGACCGGG  
 GGGTCATGGCCGTACAGCGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA  
 GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCCCTGCCCTAAAGATGTC  
 GGTCTCGAAACGAGCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG  
 AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAAAGACCAGCGACCAGGACTTCACACCT  
 GAGAAGAAAGCAGCGGTCCGGCGCCACGGAGGGGCCCTCTGGGGGACGGAAAAAAAAGAA  
 GGGCCGTAGCCTCGACTCCGACTCCAAGGCCGATTGGACGGGCCAGCCTGAGCCGG  
 TGGCCATGGCGGGTGGCGTCCCTCCCTCCCTCCCTCCCTCCCTCCGACTCCGATGTG  
 TCTGTGAAGAAGCCTCCGAGGGGCAGGAAGCCAGCGGAGAAGCCTCTCCGAAGCCCGAGG  
 GCGGAAACCGAAGCCTGAACGCCCTCCGTCCAGCAGTGACAGTGACAGCGACGAGG  
 TGGACCGCATCAGTGAGTGGAAAGCGGGGACGAGGCGGGAGCGAGCTGGAGGCCGG  
 CGCGGGCAGAGCAGGAGGAGGAGCTGGCGGCTGGGGAGCAGGAGAAGGAGGAGAAGGA  
 GCGGAGGCGCAGCGGGGCCGACCGCAGGGAGGCTGAGCGGGGAGCAGCGGGCAGCAGCGGGG  
 ACGAGCTCAGGGAGGACGATGAGCCGTCAAGAACGCGGGACGCAAGGGCGGGCGGGT  
 CCCCCGTCCCTCTGACTCCGAGCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGC  
 GAAGAACGCCGAGTCCCTCAAGCACAGAGCCGCCAGGAAACCTGCCAGAAGGAGAAGAG  
 TGCAGCCCGAGGAGAAGCAACAAGCCAAGCCGTGAAGGTGGAGCGGACCGGAAGCGGTCC  
 GAGGGCTTCGATGGACAGGAAGGTAGAGAAGAACGCTCCGTGGAGGAGAAGCT  
 GCAGAACGCTGCACAGTGAGATCAAGTTGCCCTAAAGGTCGACAGCCGGACGTGAAGAGGT  
 GCCTGAATGCCCTAGAGGAGCTGGAACCCCTGCAGGTGACCTCTCAGATCCTCCAGAAC  
 ACAGACGTGGTGGCCACCTTGAAGAAGATTGCCGTTACAAAGCGAACAGCGTAATGGA  
 GAAGGCAGCAGAACGACTATACCCGGCTCAAGTCGGGTCTCGGCCAACAGATCGAGGCCGG  
 TGCAGAAAGTGAACAAAGGCTGGATGGAGAAGGAGAAGGCCGAGGAGAACGCTGGCCGGGGAG  
 GAGCTGGCCGGGGAGGAGGCCAGGAGAACGGCGGAGGACAAGCCCAGCAGCGACGATCTC  
 AGCCCGAGTGAATGGCAGGCCACATCACAGAACGGGGAGAGCGCAGAGGACAAGGAGCAG  
 AGGAGGGTGGGACTCGGAGGGAGGGCCAAGGTGTGGCTCTGAAGACCTGCACGACAGC  
 GTACGGGAGGGTCCCGACCTGGACAGGCCTGGAGCGACCCGGAGGAGCAGGAGAGGGCAG  
 GGGGGACTCGGAGGCCCTGGACGAGGAGAGCTGAGGCCGCCAGGCCAGGCCAGCCCCGC  
 CCGAGCTCAGGCTGCCCTCTCCTCCCGCTCGCAGGAGAGCAGAGCAGAGAACGTGGG  
 GAACGCTGTGCTTTGTATTGTTCCCTGGTTTTTCTGCCTAATTCTGTGATT  
 TCCAACCAACATGAAATGACTATAAACGGTTTTAATGA

**FIGURE 174**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286  
><subunit 1 of 1, 671 aa, 1 stop  
><MW: 74317, pI: 7.61, NX(S/T): 0  
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNNKYPPIFFFGTHETAFLGPKDLFPYD  
KCKDKYKGKPNKRKGFNEGLWEIQNNPHASYSAPPVSSSDSEAPEANPADGSDADEDDEDRG  
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSLDQASVSPSE  
EENSESSSESEKTSQDFTPEKKAAVRAPRRGPLGGRKKKAPSASDSKADSDGAKPEPV  
AMARSASSSSSSSSSDSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSDSDSDEV  
DRISEWKRRDEARRREARRREQEEELRRLREQEKEEKERRERADRGEAERGSGGSSGD  
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKSAKKPQSSSTEPARKPGQKEKRV  
RPEEKQQAKPVKVERTRKRSEGFSDRKVEKKKEPSVEEKLQKLHSEIKFALKVDS PDVKRC  
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMEEKAEVYTRLKSRVLGPKIEAV  
QKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGEESAEDKEHE  
EGRDSEEGPRCGSSEDLHDSVREGPDILRPGSDRQERERARGDSEALDEES

**Signal peptide:**

amino acids 1-13

## FIGURE 175

GTGGTTCTGGATCTCACCTAACACTGCAGATCTGGACTCATCAGCCTCAATAATTATTAATTAAATTAA  
 ACACCATTGAAAGAGAACATTGTTTCATC**ATG**AATGCTAATAAGATGAAAGACTTAAAGCCAGAAGCCAAGA  
 TTTCACCTTTCTGCTTGATGATGCTAACGATGACATGACATGTTCTTCAGTCAGTCAGTCAGTCAGTCAG  
 AAATATTCAAGACTCAAGCTAACCTACAAAGACTGCTGCTTCAATAGCTGTATTCCCTTTGGGTTCATC  
 AGAAGGACTGGATTTCAAACTCTCTTAGATGAGGAAGAGGAGCTGCTCTGGGAGCAAAGACCACAT  
 CTTCTACTCAGTCTGGTGAACAAACAAATTAAAGAAGATTATTGGCTGCTGCAAAGGAACGGGTGGA  
 ATTATGTAATTAGCTGGAAAGATGCCAACAGAACATGTGCAAATTTCATCAGAGTACTTCAGCCCTATAACAA  
 AACTCACATATATGTTGGAACCTGGAGCATTCTACATCCAAATGTTGAGTATTGATCTGGAGTCTACAAGGA  
 GGATATTATATTCAAACACTAGACACACATAATTGGAGTCTGGCAGACTGAAATGTCCTTCGATCCTCAGCAGCC  
 TTTGCTCAGTAATGACAGATGAGTACCTACTCTGAAACAGCTCTGATTCTGGAAAGATACTGCATT  
 CACTCGATCCCTGGGCCTACTCATGACCACACTACAGAACACTGACATTTCAGAGCACTACTGGCTCAATGG  
 AGCAAAATTATTGAACTTCTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTCTTCTTCG  
 TGAATCATCTCAAGAAGGCAGTACCTCGATAAAACCATCTTCAGTTGAGTGAAGAGTTGTAAGAATGATGT  
 AGGAGGACAACGCAGCCTGATAAAACAAGTGGAGCAGTTCTTAAGGCCAGACTGATTGCTCAATTCTGGAAAG  
 TGATGGGGCAGATACTTACTTTGATGAGCTCAAGATATTATTACTCCCCACAAGAGATGAAAGAAATCCTGT  
 AGTATATGGAGTCTTACTACAACCAGCTCCATCTCAAAGGCTGCTGTTGAGTATAGCAGTGGCTGACAT  
 CAGAGCAGTTTAATGGTCCATATGCTCATAGGAAAGTGCAGACCATCGTTGGGTGAGTATGATGGGAGAAT  
 TCCTTATCCACGGCCTGGTACATGTCAAGCAGAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTCAGA  
 TGATGTCATCAGTTCTATAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTGCAAGGAGGACCAACGTT  
 CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCATTGCAAGAGATGGCAGTACGA  
 TGTAATGTTCTGGAAACAGACATTGGAACTGCTCTCAAAGTGTGAGCATTCTCAAAGGAAAGTGGAAATATGGA  
 AGAGGTAGTGTGGAGGAGTGCAGATATTCAAGCACTCATCAATCTTGAACATGGAATTGTCAGTCAG  
 GCAACAATTGTACATTGGTCCCGAGATGGATTAGTTCAGCTCTCCTGCACAGATGCGACACTATGGGAAAGC  
 TTGGCAGACTGTTGCTTGCAGAGACCCCTACTGTGCTGGATGGAATGCACTGCTCTGATATGCTCCTAC  
 TTCTAAAAGGAGAGCTAGCAGCCAAGATGTAATGGAACAGGCAATCACCCAGTGCTGGACATCGAAGACAG  
 CATTAGTCATGAAACTGCTGATGAAAAGGTGATTGGCATTGAATTAACTCAACCTTCTGGAATGTATACC  
 TAAATCCAACAAGCAACTATTAAATGGTATATCCAGAGGTCAAGGGATGAGCATCGAGAGGAGTTGAAAGCCCAG  
 TGAAAGAATCATCAAACCGAATATGGCTACTGATTGAAAGTTGCAAGAGAAGGATTCTGGATGTTACTG  
 CAAAGCCCAGGAGCACACTTCATCCACACCAGTAGTGAAAGCTGACTTGAATGTCATTGAGAATGAAACAGATGGA  
 AAATACCCAGAGGGCAGAGCATGAGGAGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTGAGATACAAAGA  
 CTACATCCAATCTTAGCAGCCAAACTTCAGCCTCGACAGACTGCGAACAGATGTGGCACAGGGAGAAGCG  
 GAGACAGAGAAACAAGGGGGCCAAAGTGGAAAGCACATGCAAGGAAATGAAAGAAGAAACGAAATGAAAGACATCA  
 CAGAGACCTGGATGAGCTCCCTAGAGCTGAGCCACG**TAG**TTTCTACTTAATTAAAGAAAAGATTCTTAC  
 TATAAAAACATTGCTCTGTTGATATCCCTTATAGTAAATTCTAAATGCTTCCATGGAGTTGCTAAGG  
 CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAATTCTATGAAACCAGTT  
 CCAAGAACAAATCTGCAAGCAAAGTATAAGAATTCTCTAAAATAGGGGGTTACAGTTGTAATGTT  
 TGTTTGAGTTTGGAAATTATTGTCATGTAATAGTTGAGCTAAGCAAGCAGCCGAATTGAGTGTATAAGGT  
 GCTTATTCCCTCGAATGTCATTAAGCATGGAATTACCATGCAAGTTGCTATGTTCTATGAAACAGATAT  
 CATTCTATTGAGAACCGAGCTACCTGTGGTAGGGATAAGAGGTCAAGACACAAATTAAAGACAACCTCCATTATC  
 AACAGGAACCTCTCAGTGAGGCATTCACTCCTGGAGAATGGTATAGGAATTGGAGAGGTGCAATTCTT  
 TGGCCACTGGGGTAAATTAGTGTACTACACACATTGATTACTGAAGGGCAATTGTTCCCCCAGGATTCT  
 ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTGGTCTTAGTTATGTTTTAGAGTATATACTAA  
 GCTCTACAGGGACAGAACGTTAAATAATCTTAATAAGATATGGAAAATTCTTAATAAAACAAGGAAAACA  
 TAATGATGTTATAATGCACTCTGATGGAGGGCATGCAAGATGGATTGTTAGAAGACAGAAGGAAAGACAGCCAT  
 AAATTCTGGCTTGGGGAAACTCATATCCCCATGAAAAGGAAGAACATCACAAATAAGTGGAGTAATGTA  
 TGGAGCTCTTCACTAGGGTATAAGTAGCTGCCAATTGTAATTCTGTTAAAAAAATCTAGATTATAACA  
 AACTGCTAGCAAATCTGAGGAAACATAATTCTCTGAAAGAACATAGGAAGAGTAGACATTATTTATAACC  
 AATGATATTCTAGTATATATTCTCTCTTTAAAAAATTATCTACTCTGTATATTATTCTTTACTGC  
 CTTTATTCTCCTGTATATTGGATTTGTGATTATTTGAGTGAATAGGAGAAACAATATAACACACAGA  
 GAATTAAGAAAATGACATTCTGGGAGTGGGATATATTGTTGAATAACAGAACGAGTGTAAAATTAAAC  
 AACGGAAAGGGTTAAATTAAACTCTTGACATCTCACTCAACCTTCTCATTGCTGAGTTAATCTGTTGAATT  
 GTAGTATTGTTTGTAAATTAAACAATAAAAGCCTGCTACATGT

**FIGURE 176**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLQNIPLRKLYKDLLLSNSCIPFL
GSSEGLDFQTLLLDEERGRLLLGAKDHFIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAHPICGYIDLGVYKEDIIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDFKTLISRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCAKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSIKEKWNMEEVLE
LQIFKHSSIIINMELSLKQQQLYIGSRDGLVQLSLHRCDTYKACADCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHTADEKVIFGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRNRHRLDELPRAVAT
```

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

## FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTATCCTGGAGCATGCCACCAGCGGGGAGCAGA  
 CAAACCTCCCAGGTAAAGCTGGGAGCAAGACCTGAAGCTGTTCTCAGGAGCCTGGTGTATTTCACCCACCCAC  
 CTCAGCAGTTTCAGCCACAGGGACTGATCAGGTGTGCTCTGGAGTGGGAGCAGAAGGGTGGCTGGCAAGA  
 GTGGCCTGGAGAAAGAGGTTCAAGCGCTTGACCAGCGAGCTGCCGTGACTACAAGATCCAGAACCATGGGCATC  
 GGGTGAGGTGGGGGGCACAGGTGTATGTGACCTTCTGTCAAGCAAGAAGAGCTGAGAGAGGGATCTTGG  
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGAGGGAAAGGTATTTAAGGTAACAGTGTGGCACAATAGTTAA  
 GAGCACAGTTTGAGCTAGACCGACATAGGTCAAAATTCTCTTCTGTGCTCTAGTCTGTAGCCCCAGGT  
 AAGGGAGTGACTTAACCTCTGGACTTCATCAATTCTCATCAACTAAAGTAGGGCCAATAATAGCACCCACCTCAT  
 AGGGAAAGATTAATGACATAATGTATGT**ATG**CAACTAGCAAAGTACCCAGTCCCATAGTAAGTCATGCCACAG  
 TATTCCACCCACCCCTGTTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGCGGAGCAGGCTT  
 CAGAGCGGGAGGCTCAAGCATAGAACAGAGGTACAGGAAGTGCAGAGAGCATCGCCGGGACAGGTGAGCC  
 AGGTGAAGGGGCTGCCGGCTGGCCCTGCTGCAGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA  
 TGACCCAGGCCAGGATGAGGTGGAGCAGGAGGGCGGCTCAGTGAGGCTCGGCTGTCAGGAGCTTCTGAGGAGC  
 CAACCGCTGAGGATGCTGAGCTTCTGACTTGAGGAATGTGAGGAGACGGGAGAGCTCTTGAGGAGCCTGCC  
 CCCAAGCCCTGGCACGAGGCCCTCCCTGCCCTGCACACGTGGTATTCGCTATCAGGAGGGCTGAGGATG  
 AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTATAGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA  
 ACCAGCACGGCGAGGTAGGCTTGTCCCTGAGCGATATCTCAACTTCCCGACCTCTCCCTCCAGAGAGCAGCC  
 AAGACAGTGACAATCCCTGCGGGCAGAGCCCACAGCATTCTGCACAGGCCCTGTACAGTACACCGGACAGA  
 GTGAGAGGAGCTGAGCTCCCTGAGGGGCACTCATCCGTCTGTCGCCCCGGCCAAGATGGAGTAGATGACG  
 GCTTCTGGAGGGGAGAATTGGGGCCGTGTTGGGTCTCCCCCTCCCTGCTGGTGGAGAGCTGCTTGGCCCC  
 CAGGGCACCTGAACTCTGACCCCTGAACAGATGTCGCGTCCCCCTCTCTCCCGACCTCTCCCCACCTGCAC  
 CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTGCTGGCTGGGACAAGGCTGGACTTCCCTGGTTCTGG  
 ACATGATGGCACCTGACTCAGGCCATGCGTCCACCACCTCCCGGGCTAAAGGCCCCGATCTGGCCACC  
 CAGATCCCCCTACCT**TGA**AGGCCAGGGAGCCTGAAAGCCCTGATGCTGCTGTCCTATCTCAAGCTGTCA  
 CCACACCATCAATGATCCAGAGCAACACAGCCAAAGCTGGAACCTGCCCCCTATTCCACCCCTCACCTCAAGGGT  
 GGAAACTTGCCCCCTCCCATTTCTAGAGCTGGAACCCACTCTTTTTTCCATTGTTCTATCATCTAGGACC  
 GGAACTACTACCTCTCTGTATGACCCCTATCTAGGGTGGTGAATGCCTGAATCTGGGCTGGAAACC  
 ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTCCCCACCCCTGGCTCATGACCCACCCACTCTGGATG  
 CCAGGGTCACTGGGTTGGCTGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAGGCCAGGATGCGAAGCAG  
 CTGTAATGGCTGAGCGGATTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCTGGCCCTTGTG  
 CTAAGAGGGCAGGGGCCACGGTCTATTGCTTAGGGGCCACACGGCAGGGGCTGTCCTGGCAG  
 GCTCTATCATATGGAGCGAGGTGTTGGGAAGGGGGCAGGCAGCCTGTTGCAAGGAGGGAAAGGAGAGAC  
 TGAGGGCTGTGACCTCTCTGAGGCCAGGCTGAGACTGTGCAACTCCAGGTGGAGAGCTGGTCCCT  
 AGCTGGGGGAGTGTGTCAGTGGAGGGAGGGCTTCACGCCACCCACCCCTGGCCCTGCCAGCTGGTAG  
 TCCATCAGCACAAATGAAGGAGACTGGAGAAGAGGAAGATAACACTGTTGCTCTGTGTCAGCTGTG  
 TTTCCCTGGGCTCCAGGACCTCCACCAACCAAGGGATTATAGCAAAGGCTAACGCT  
 AGTTTACTCTGGGGTTCAAGGAGGCCAAAGGCTAAATAGTTAAGTAGGTGATGGGAAGATGAGATTACCTCA  
 TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGAGACACCTGAGAGAAAGGGGG  
 TCAACAATGAGAGACCCAGGAGTAGGTCTATCAGTGGCCCCCAGAGTAGAGAGGAATAAGGCCAGGCCAGTGC  
 AGTCCCGGCTGTGTTCTACCTGGTGTAGAAGTGTCTGGTTGCTGGCTGCCATTGCGCTTCAAGTGG  
 GCAGGCCCTGGGCTTGGGCCCCCTCCCGGGCTCAGTGTGGCTCTGCCAGAACGCTCTGGGTTCCCTCAAGTG  
 CACGGGGGTTAGGGCTGTGCTCCCTGAGTCCTCATTCTGTACTGGGGGCTGGCTAGGACCTGGGCTGTGGCC  
 TCTCAGGGGCCAGCCTCTCCATGGCAGGCATCCCTGCCTGGCTGCCCTCCCCAGACCCCTGACCCACCCCTG  
 GGTCTGTCCCCCACCAGAGCCCCAGCTCTGTGTGGGGAGGCCATCACGGTGTGTCAGTCCATAGCGCT  
 TCTCAATGTGTGTCACCCGGAACCTGGAGGGAGGGAAACTGGGTTAGGACCAACTCAGAGGCTGTTG  
 GCCCTCCCTCTGACCAAGGGACATCTGAGTTGGCTACTTCCCTCTGGCTAACGGTAGGGAGGCCCTCTC  
 AGATTGTGGGGCACATTGTGAGCCTGACTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGGCCAACGGCCACTT  
 TTGGGATCAGGTGCTGATCACTGGCCCCCTACCTCAGCCCCCTTCCCTGAGCAGCTGCCACCTGCCCA  
 CAGAGAACACAGTGGCTCCCTGTCCGGGGCGGTTTCTCTGGAGCAGCTGCCACCTGCCCA  
 GCCTCTGCTCGGGCTGCAATGGATGCAAGGGCTGCAGAGGCCAGGTGCACTGTGATGATGGGAGGGGCTC  
 CGTCTGCAAGGCTGGAGGTGGCATCCACACTGGACAGCAGCAGGAGGGAGTGAAGGTAACATTCCATT  
 TCATGTTTGTCTTACGTTCTGCACTGCTCTTAAACCCAGAACGCCAACCTCCAAAGGCCATT  
 TTTCTGTCTTATCTAATAACTCAATATTAAG

**FIGURE 178**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401  
><subunit 1 of 1, 370 aa, 1 stop  
><MW: 40685, pI: 4.53, NX(S/T): 0  
MQLAKYQSHSKSCPTVFPPTTVLCLPNQVLQRTLEQRRQQASEREAPSIEQRLQEVRESIRRA  
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS  
DFEECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTITEGEWLEVIEEGDADEW  
VKARNQHGEVGFVPERYLNFPDLSLPTESSQDSDNPCGATPTAFLAQALYSYTGQSAEELSFP  
EGALIRLLPRAQDGTVDDGFWRGEFGGRGVFPTSLVEELLGPPGPPTELSDPEQMLPSPSPPS  
FSPPAPTSVLDGPPAPVLPTGDTKALDFPGFLDMMATPRLRPMRPPPPPAKAPDPGTHPDPLT

## FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAGAGAGACAGAGACAAAGGCACAGCGGAA  
 GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCAGACAGAGTCCTACAGAGGGAGAGGCCAGAGAACGTCAGA  
 AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTGGAGAGGCCAGAGAACGTCAGA  
 GCACCTCTCCCAAGCCAAGGACTAAGTTCTCCATTCTTAAACGGTCTCAGCCCTCTGAAAACCTTGCC  
 TCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTCAAAGCTAGGGTGTGGAGGACTTGGT  
 GCCCTAGACGGCCTCAGTCCCTCCAGTGCAGTACCGTGC**ATG**CCCAGACAGGCTCGCATCCGGGAGGGG  
 CTTGGCAGGGCGCTGGCTGGGGAGCCAAACCTGCCTCTGCTCCCCATTGTGCCGCTCTCTGGCTGGTGTG  
 GCTGCTTCTGCTACTGCTGGCTCTGCTGCCAGCCGGCTGGCCAGCCCCCTCCCCGGGAGGAGGAGAT  
 CGTGTTCAGAGAAGCTAACGGCAGCGTCTGACTAGAGCTGGAGCAGGACTCCGGTGTGCAAGGTGAGGGCTGACAGTGCAGTA  
 GGCCTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAAGGTGAGGGCTGACAGTGCAGTA  
 CCTGGGCCAGGCGCTGAGCTGCTGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC  
 GGAGTCGGTGGCATCTGCACGGGATGGGGAGCCCTGTTAGGCGTGTACAATATCGGGGGCTGAACTCCA  
 CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACCTGCTGGGGACCTGGGGCTCACATCCTACGCCGGAAAGAGTCC  
 TGCCAGCGGTCAAGGTCCTAGTGCACAGTCAGGCTCCTCTGGAAGCCCCAGGCCAGACCCGAAGAGCCAA  
 GCGCTTGCCTCACTGAGTAGATTGTGGAGACACTGGTGTGGCAGATGACAAGATGCCGATTCCACGGTGC  
 GGGGCTAAAGCGTACCTGCTAACAGTGTGGCAGCAGCAGGCCAAGGCCCTCAAGCACCCAGCATTCCACGCAATCC  
 TGTCAGCTTGGTGGTGAECTGGCTAGTGTGATCTGGGTCAGGCGAGGGGGCCCAAGTGGGGCCAGTGTG  
 CCAGACCCCTGGCAGCTCTGTCGCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA  
 CACAGCCTTGTGACCCGGCTGGAGCTGTGCCATTGTGGAGGATGATGGGCTTCACTGCGACACGCTGGTATGGTGTG  
 CACCGTCTGTGACCCGGCTGGAGCTGTGCCATTGTGGAGGATGATGGGCTTCACTGCGACACGCTGGTATGGTGTG  
 TGAACGGGTCACTGCTTCAACATGCTCATGGACACTCAAGCCATGCACTGTTGAATGGGCTTGTGAGCAC  
 CTCTCGCCATGTCATGGGCCCTGTGATGGCTCATGGTGGAGGCTGGTGGGACCTGGGCTTGTGAGTGGCCCTTGCAGTGGCCGCTT  
 CATCACTGACTTCTGGACAATGGCTATGGCAGTCTGCTTGTAGACAAACAGAGGCTTCACTGCGACACGCTGG  
 GACTTCTCTGGCAAGGACTATGATGCTGACCCGCACTGCCAGCTGACCTTCGGGCGACTCACGCCATTGTCC  
 ACAGCTGCCGCCCTGTGCTGCCCTCTGGTGTCTGGCACCTCAATGGCATGCCATGTGCCAGACCAAACA  
 CTCGCCCTGGCGATGGCACACCCCTGGGGCCGACAGGCCATGGGTGGCTGCCACATGGACCA  
 GCTCCAGGACTCAATATCCACAGGCTGGTGGCTGGGCTTGGGACCATGGGTGACTGCTCTGGACCTG  
 TGGGGTGGTGTCCAGTCTCTCCCGAGACTGCACGAGGCCCTGCCCCGGAAATGGTGGCAAGTACTGTGAGGG  
 CGCCGTACCCGCTCCGCTCTGCAACACTGAGGACTGCCAAGCTGGCTAGCCCTGACCTCCGCGAGGAGCA  
 GTGTGCTGCCATAACCACCGCACCGACCTCTCAAGAGCTTCCAGGGCCATGGACTGGGCTCTGCTACAC  
 AGGCGTGGCCCCCAGGACAGTGCACAAACTCACCTGCCAGGCCGGACTGGCTACTACTATGTGCTGGAGCC  
 ACGGGTGGTAGATGGGACCCCTGTCCCCGGACAGCTCTGGTGTGTCAGGGCGATGCATCCATGCTGG  
 CTGTGATGCATATTGGCTCCAAGAAGAAGTTGACAAGTGCATGGTGTGCCAGGGGACGGTTCTGGTGTG  
 CAAGCAGTCAGGCTCCTTCAGGAAATTAGGTACGGATAACAACATGTGGTCACTATCCCCGGGGGCCACCCA  
 CATTCTTGTCCGGCAGCAGGGAAACCTGGCACCGGAGCATCTACTTGGCCCTGAAGGCTGCCAGATGGCTCTA  
 TGCCCTCAATGGTGAATAACGCTGATGCCCTCCCCACAGATGTGTACTGCCCTGGGCACTGCCCTTGACACTGCAAGTCT  
 CAGCGGGGCCACTGCAGCTCAGAGACACTGTGAGGCCATGGGCCACTGCCCTTGACACTGCAAGTCT  
 AGTGGCTGGCAACCCCCAGGACACACGCTCCGATACAGCTTCTGGTGTGCCCCGGCACCCCTAACGCCACG  
 CCCACTCCCCAGGACTGGCTGACCGAAGAGCACAGATTCTGGAGATCCTGGCGGCGCCCCCTGGCGGGAG  
 GAAA**TAA**CTCACTATCCGGCTGCCCTTCTGGCACCGGGCTCGGACTTAGCTGGAGAAAGAGAGAGCTT  
 CTGTTGCTGCCCTATGCTAAGACTCAGTGGGGAGGGCTGTGGGCTGAGACCTGCCCTCTCTGCCCTAAT  
 GCGCAGGGCTGGCCCTGCCCTGGTTCTGCCCTGGGAGGGCAGTGTGGTTAGGGATGGAAGGGCTGACAGAC  
 AGCCCTCCATCTAAACTGCCCTCTGCCCTGCCCTGGGTCACAGGAGGGAGGGAGGGCAGGGAGGGCTGGGCC  
 CAGTTGTATTATTAGTATTCTACTTTTATTAGCACCGAGGAAAGGGACAAGGACTAGGGTCTGGGAA  
 CCTGACCCCTGACCCCTCATGCCCTACCGCTGGGCTAGGAAATCCAGGGTGGTGTAGGTATAAGGGT  
 TGTGTATGCGTGTGTGTGAAAATGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTCT  
 TTCTCTGAATTATTATTAGTATTCTCTTCTTTCTTTCTGGAGACAGAATCTGCTCTGCGCCAGGCTGGAGTGC  
 GCACAACTCGGCTCACTGCATCCTCCGCCCTGGGTCAGTGTGATTCTCATGCCCTGCCCTGAGTAGCTG  
 GGATTACAGGGCTGCCACCAGGCCAGCTAATTGGTTGTTGGAGACAGAGTCTCGCTATTGTC  
 ACCAGGGCTGGAATGATTCACTGCAACCTTCGCCACCTGGGTTCCAGCAATTCTCTGCCCTAGCCTCC  
 CGAGTAGCTGAGATTAGGCACCTACCACGCCGGTAATTGGTATTTAGTAGAGACAGGGTTCAC  
 CATGTTGGCCAGGCTGGTCTGAACTCCTGACCTAGGTGATCCACTGCCCTCATCTCCAAAGTGTGGGATT  
 ACAGGGCTGAGGCCACCGTGCCTGGCACGCCAACTAATTGGTATTTAGTAGAGACAGGGTTCACCATGT  
 TGGCCAGGCTGCTCTGAACTCCTGACCTCAGTAATCGACCTGCCCTGCCCTCCAAAGTGTGGGATTACAGG  
 TGTGAGGCCACCACGCCGGTACATATTAAATTGAATTCTACTATTATGTGATCCTTGGAGTCAGACAG

## **FIGURE 179B**

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTCTCATTGCCAATAATAATACCTCCCTTAGAAG  
TTTGTGTGAGGATTAATAATGTAATAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAGGAAA  
AAAAAAAAAAAAAAAAGGAAA

## FIGURE 180

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLASLLPSARLASPLPREEEIV
FPEKLNGLVPGSGAPARLLCRLQAFGETLLEQDGSVQVEGLTVQYLGQAPELLGGAEP
GTYLTGTINGDPESVASLHWDGALLGVLQYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPMCNVKAPLGSPSPRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAFKHPSIRNPVSLVVTRILVILGSGEEGPQVGPSSAQTLSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHD
NSKPCISLNGPLSTSRRHMAPVMAHVDPPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFPGKDYDADRQCQLTGPDSRHCPCQLPPPACAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNIPQAGGWGPWGPWGDCSRCTGGGVQFSSRDCTRVPVRNGGKY
CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMWDWVPRYTGVAPQDQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPQDWLHRRAQILEILRRRPWAGRK

```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 358-367

**FIGURE 181**

CAGCAGTGGTCTCTCAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**  
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTAAATCC  
AAGAAAATATGTAAATCACTTAAGATTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT  
AATTGTCTGTTGGGGAGCAAGCAGTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTG  
ACCAGAACTGAAATATTAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
TAAAAACGGATACACTGGCATCTACTTCGTGGTCTTCAAAAATGTTTATCAAAACTCAGA  
TTAAAGTGATTCTGAATTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
ACAACCTTCTTGAACAGTCAGTGATTGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
TTTCTTAAAAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC  
CCACTCTAATATCAGTTCTGAGTTACAAGACTTGAGGAGGGAGAAGATCTTCACTTT  
CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAGT  
AGAGAAGACCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCAATAATGACTATACTG  
AAAATGGAATAGAATTGATCCCAGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT  
CGAGGCAACCGCTATTGCCGCCGCTGTGAACCTTACTAGGCTACTACCCATATCCATA  
CTGCTACCAAGGAGGACGAGTCATCTGCGTGTACATGCCCTGTAAGTGGTGGTGGCCC  
GCATGCTGGGGAGGGC**TAA**AGGAGGTTGAGCTCAAATGCTAAACTGCTGGCAACATAT  
AATAATGCATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT  
CTCCAGAATTACTGTAGGTAATTCTCTCTTCATGTTCTAATAACTTCTACATTATCACC  
AAAAAAAAAAAAAAAAAA

## **FIGURE 182**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLIVLFWGSKHF
WPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDF
KNGYTGIYFVGLQKCFIKTQIKVIPEFSEPEEEIDENEIITTFEQSVI
WPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSELQDFEEEGED
LHF PAN EKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIE
FDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIM
PCNWWVARMLGRV
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

## **FIGURE 183**

GCAGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGCGTGACCCCGAGGGCCCAGGGAGCTGCC  
 CGGCTGGCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCGTGCAGCTCTGGGCTTCCT  
 GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA  
 CAGCGCACGTGGGCACCAACATCCTCACGGCGTGTACCTGAAAGGGCTCTGGATGGAG  
 TGTGTGTGGCACAGCACAGGCATCTACCAAGTGCAGATCTACCGATCCCTGCTGGCGCTGCC  
 CCAAGACCTCCAGGCTGCCGCCCTCATGGTCATCTCCTGCCTGCTCTGGGCATAGCCT  
 GCGCTGCCGTATCGGGATGAAGTGCACCGCCTGCCAAGGGCACACCCGCCAAGACC  
 ACCTTGCCATCCTCGCGGCACCCCTTCATCCTGGCCGGCCTCTGTGCATGGTGGCGT  
 CTCCCTGGACCAACGACGTGGTCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA  
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGCCCTCGCTATTGGT  
 GGCACCCCTGCTTGCCCTGCCAGGACGAGGCACCCCTACAGGCCCTACAGGCCCTACAGGCC  
 CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
 ACAATGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGTACAGGCTGAACGACTACGTG  
TGAGTCCCCACAGCCTGCTTCTCCCTGGCTGCTGTGGCTGGTCCCCGGCGGACTGTC  
 AATGGAGGCAGGGGTTCCAGCACAAAGTTACTTCTGGCAATTGTATCCAAGGAAATA  
 ATGTGAATGCGAGGAAATGTCTTAGAGGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA  
 AGCTCTCTATACCAAAGACTGAAAAAAATCCTGTCTGTTTGATTTATTATATATAT  
 TTATGTGGGTGATTGATAACAAGTTAATATAAAGTGACTTGGAGTTGGTCAGTGGGT  
 TGGTTGTGATCCAGGAATAAACCTGGATGTGGCTGTTATGAAAAAA

## **FIGURE 184**

MASTAVQLLGFLLSFLGMVGLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKTPAKTFAILGGTL  
FILAGLLCMVAWSWTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ  
DEAPYRPyQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSAHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

## FIGURE 185

GAGCTCCCTCAGGAGCGCGTAGCTCACACCTCGGCAGCAGGAGGGCGGCAGCTCTCG  
 CAGGCAGGGCGGGCGGCCAGGAT**ATG**TCCACCAACATGCCAAGTGGTGGCGTTCC  
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGGGCACCAGGATGGACATGTGGAGCACCC  
 AGGACCTGTACGACAACCCGTCACCTCCGTGTTCCAGTACGAAGGGCTGGAGGAGCTGC  
 GTGAGGCAGAGTTCAGGCTCACCGAATGCAGGCCATTTCACCACATCCTGGACTCCAGC  
 CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGTGCCATTGCCCTCC  
 TGGTATCCATCTTGCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
 AACATGACACTGACCTCCGGGATCATGTTCATTGTCTCAGGTCTTGTGCAATTGCTGGAGT  
 GTCTGTGTTGCCAACATGCTGGTACTAACTTCTGGATGTCCACAGCTAACATGTACACCG  
 GCATGGGTGGGATGGTGCAGACTGTTCAGACCAGGTACACATTGGTGCAGCTGTG  
 GGCTGGGTGCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGG  
 CCTGGCACCAGAACAAACTACAAAGCCGTTCTTATCATGCCCTCAGGCCACAGTGGT  
 CCTACAAGCCTGGAGGCTCAAGGCCAGCACTGGCTTGGGTCCAACACACAAAAACAAGAAG  
 ATATACGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTTATCCTCCAAGCACGACTA  
 TGTG**TAAT**GCTCTAACAGACCTCTCAGCACGGGCGGAAGAAACTCCGGAGAGCTACCCAAAA  
 AACAAAGGAGATCCCCTAGATTCTTCTTGACTCACAGCTGGAAAGTTAGAAAAGC  
 CTCGATTCATCTTGGAGAGGCCAAATGGTCTAGCCTCAGTCTGTCTAAATATTCC  
 ACCATAAAACAGCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTTCATCCTCTAT  
 TTCTTTTTAAATATAACTTCTACTCTGATGAGAGAATGTGGTTAATCTCTCTCAC  
 ATTTGATGATTAGACAGACTCCCCCTTCCCTCTAGTCATAAAACCCATTGATGATCTA  
 TTTCCAGCTTATCCCCAACAAAACCTTGAAAGGAAAGAGTAGACCCAAAGATGTTATT  
 CTGCTGTTGAATTGTCTCCCCACCCCAACTGGCTAGTAATAAACACTACTGAAGAA  
 GAAGCAATAAGAGAACAGATATTGTAATCTCTCCAGCCCAGTCTCGGTTTCTACACTG  
 TGATCTAAAAGTTACCAACCAAGTCATTTCAGTTGAGGCAACCAACCTTCTACTG  
 CTGTTGACATCTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAG  
 TCCTCTTCTGCGGGTCAGAAATTGTCCTAGATGAATGAGAAAATTATTTTTAAT  
 TTAAGTCCTAAATATAGTAAAATAATGTTTAGTAAAATGATACTATCTCTGTGA  
 AATAGCCTACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTGACATTGTCT  
 ATATGGTACTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC  
 CTAGCACTTGGAGGCTGAGGAGGAAGGATCACTTGAGGCCAGAAGTTCGAGACTAGCCTG  
 GGCAACATGGAGAACCCCTGTCTCACAAATAACAGAGAGAAAAATCAGCCAGTCATGGT  
 GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTGAGCCCAGGG  
 AGGTTGGGCTGCAGTGAGCCATGATCACACCAGTCAGCCAGGTGACATAGCGAGA  
 TCCTGTCTAAAAAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA  
 ACTAATTCTTAA

## **FIGURE 186**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pi: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSFVANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGVWAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV
```

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## **FIGURE 187**

GGAAAAACTGTTCTCTGGCACAGAGAACCCGCTTCAAAGCAGAAGTAGCAGTCCG  
GAGTCCAGCTGGCTAAACTCATCCCAGAGGATAATGGCACCCATGCCTAGAAATCGCTG  
GGCTTTCTGGTGGTGGATGGTGGCACAGTGGCTGTCAGTGCATGCCTCAGTGG  
AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTGAAAACCTCTGGGAAGGACTGTG  
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAACTATGATCCCTGCTGG  
CTCTTCTCCGGACCTACAGGCAGGCCAGAGGACTGATGTGCTGCTCCGTGATGTCCTTC  
TTGGCTTCATGATGCCATCCTGGCATGAAATGCACCAAGGTGCACGGGGACAATGAGAA  
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGCATGGTGGTGC  
TCATCCCTGTGAGCTGGGTGCCATGCCATCATCAGAGATTCTATAACTCAATAGTGAAT  
GTTGCCAAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCACTGGTGC  
GATTGTTGGAGGAGCTGTTCTGCTGCCTTTGTTGCAACGAAAAGAGCAGTAGCTACA  
GATACTCGATACTTCCACATCGACAACCCAAAAAGTTATCACACCGGAAAGAAGTCACCG  
AGCGTCACTCCAGAAGTCAGTATGTGTAGTGTATGTTTTAACTTACTATAAGC  
CATGCAAATGACAAAAATCTATATTACTTCTCAAAATGGACCCAAAGAAACTTGATTAA  
CTGTTCTTAACGCTTAATCTAATTACAGGAACGTGCATCAGCTATTTATGATTCTATAA  
GCTATTCAGCAGAATGAGATATTAAACCAATGCTTGATTGTTCTAGAAAGTATAGTAAT  
TTGTTTCTAAGGTGGTCAAGCATCTACTCTTTATCATTACTTCAAAATGACATGCT  
AAAGACTGCATTATTTACTACTGTAATTCTCCACGACATAGCATTATGTACATAGATGAG  
TGTAACTTATATCTCACATAGAGACATGCTTATATGGTTTATTTAAAATGAAATGCCAG  
TCCATTACACTGAATAATAGAACTCAACTATTGCTTTCAGGGAAATCATGGATAGGTTG  
AAGAAGGTTACTATTAATTGTTAAAACAGCTTAGGGATTAATGTCCTCATTATAATGA  
AGATTAATGAAGGCTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATATGCTG  
TTTTTAGCCTAGGAGTTAGAAATCTAACCTTCTTATCCTCTCCAGAGGCTTTTT  
TTCTGTGTATTAAATTAAACATTAAACGAGATATTGTCAGGGCTTGCATTCA  
AACTGCTTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTG  
GTTTAGGAAAGTGAAAATATTTGTTTGTATTGAAGAAGAATGATGCATTGACAA  
GAAATCATATATGTATGGATATATTAAATAAGTATTGAGTACAGACTTGAGGTTCATC  
AATATAAAATAAGAGCAGAAAAATGTCTGGTTTCATTGCTTACCAAAAAACAAACA  
ACAAAAAAAGTTGTCCTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTC  
AACTGCTTCTGTGAAAATAAAATTCTTCTGTGACCTTCTGTCATTGTTAGTTACTAA  
ATCTGTAATACTGTATTCTGTTATTCCAAATTGATGAAACTGACAATCCAATTG  
AAGTTGTCAGCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTATACATTATA  
TTAATAAAATTGTACATTCTAATT

## **FIGURE 188**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV
```

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## **FIGURE 189**

TCGCC**ATG**GCCTCTGCCCGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCATGTGGAAGGTGACCGCTTCATCGGCAACAGCAT  
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC  
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGTGCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTCATGCCCTCCTGTGGCCCTGTTGGCTGCTGGTCTACCTTGCTGGGC  
CAAGTGTACCACCTGTGGAGGAGAAGGATTCCAAGGCCCGCTGGTGCACCTCTGGGA  
TTGTCTTGTCACTCAGGGTCTGACGCTAATCCCCGTGCTGGACGGCGATGCCATC  
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCAAAAGCGGGAGCTGGGGCCTCCCT  
CTACTTGGGCTGGCGGCCCTCAGGCCTTGTGCTGGTGGGGGTTGCTGTGCTGCACTT  
GCCCTCGGGGGGGTCCAGGGCCCCAGCCATTACATGCCCGCTACTAACATCTGCCCT  
GCCATCTCTCGGGGGCCCTGAGTACCCCTACCAAGAATTACGTC**TGA**CGTGGAGGGAAATG  
GGGGCTCCGCTGGCGCTAGGCCATCCAGAAAGTGGCAGTGCCAACAGCTTGGATGGTT  
CGTACCTTTGTTCTGCCCTGCTATTCTTGTGACTGAGGATATTAAAATTCAATT  
GAAAATGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTGCTGTTCTCACCTTGG  
ATGATGGAGCCAAGAGGGATGCTTGAGATTCTGGATCTGACATGCCATCTAGAAC  
CAGTCAAGCTATGGAACATGCGGAGGCTGCTGCTGTGCTGGCTTGCAACAAGACAGAC  
TGTCCCCAAGAGTTCTGCTGCTGGGCTGGCTCCCTAGATGTCAGTGGACAGCTG  
CCCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTTCACCCCTGGAAAAACAAATCATCTG  
TTAACAAAGGACTGCCACCTCCGAACTTCTGACCTCTGTTCTCCGTGATAAGACG  
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCTCGTCTCACCCCTTACACTCACATTATCAAATAAGCATG  
TTTGTAGTGCA

## **FIGURE 190**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTS
GIVFVISGVTLIIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLC
TCPGGSQGPGSHMARYSTSAPAISRGPSEYPTKNYV
```

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

## **FIGURE 191**

GCCAAGGAGAACATCATCAAAGACTTCTAGACTCAAAAGGCTTCCACGTTCTACATCTTGA  
AGCATCTTCTACCACTCCGAATTGAACCAGTCTCAAAGTAAAGGCAATGGCATTATCCCTT  
TTGCAAATTGCTGGCTGGTCTGGGTTGCCATGGTGGGACTCTGCCACAAACCT  
TCTGCCTCAGTGGTGGAGTATCAGCTTGTGGCAGCAACATTATTGTCTTGAGAGGCTC  
TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTGCAATGCAAGTTCTA  
TAGCTCCTTGTGGCTCTCCGCCTGCCCTGGAAACAGCCCGGCCCTCATGTGTGTGGCTG  
TTGCTCTCTCCTTGATGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
GGCTCTAACGAGAGGGCAAAGCATACTTCTGGAACTTCAGGAGTCCTCTCATCCTGAC  
GGGTATCTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA  
ACCCAGCCATCCACATAGGTAGAAACGAGAGCTGGAGCAGCACTTTCTGGCTGGCA  
AGCGCTGCTGTCCTCTCATTGGAGGGGTCTGCTTGTGGATTTGCTGCTGCAACAGAAA  
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTAATGCCTCCTTGGCTCCAAGT  
ATGGACTATGGCAATGTTTATAAAGCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA  
GAACCTGCTTATGTCTAGATTACATTGATACGAAAGTTCAATTGTTACTGGTGGTAGG  
AATGAAAATGACTTACTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
GACCCAATCGCTGCTCCAATTTCATATTCTAAATTCAAGTATAACCCATAATCATTAGCAAG  
TGTACAATGATGGACTACTTATTACTTTGACCATCATGTATTATCTGATAAGAATCTAAA  
GTTGAAATTGATATTCTATAACAATAACATACCTATTCTA

## **FIGURE 192**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPIPVSWTANIIIRDYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV
```

**Important features of the protein:**

**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

**FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTCCAGCATGAAGATCACTGGGGT  
CTCCTTCTGCTCTGTACAGTGGTCTATTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
AAAAAAAGTGGACTGCAGCATTACAAGAAGTATCCAGTGGTGGCCATCCCCATGCCCATCA  
CATACCTACCAGTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC  
GAGAGCTTGAAAAGTAATGGAAGAGTCAGTTCTTCACGATGGAAGTTGCTAAATTCTCCA  
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG  
AGTTTCTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAAGAGTAATCTTG  
ACTGAATGGAGAAAGTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
TTTTTTTTAACACGTCAATAAAAAATAATCTCCCAGA

## **FIGURE 194**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC
```

**Signal peptide:**

amino acids 1-19

**FIGURE 195**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC  
CGCCGCCATGGCTGCCTCCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGCCCAGGTGGCATAAGTGGAAATAACTCAAGCTGATGCTTCAA  
AAACGAGAAGCACCTGTTCCAACTAAGACTAAAGTGGCGTTGATGAGAATAAAGCCAAAGA  
ATTCCTTGGCAGCCTGAAGCGCCAGAACGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGC  
AGCAGTGGTACCAGCAGTTCTACATGGGCTTGATGAAGCGAAATTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCTACGGCTTAGGCATGGAGGCCAGCG  
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT  
TCTTCATGTATCTCCTAACCGCTTACACTACTTGGTTCTGATTGCTCTATTCAGCAGAT  
CTTTCTACCTACTTGTGTGATCAAAAAGAAGAGTTAAAACACATGTAAATGCCTTT  
TGATATTCATGGGAATGCCTCTCATTAAAAATAGAAATAAAGCATTGTTAAAAGA

## **FIGURE 196**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLLCWGP GGISGNKLKMLQKREAPVPTKTKAVDENAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDYYQRHYD
EDSAIGPRSPYGF RHGASVNYDDY
```

**Signal peptide:**

amino acids 1-30

## **FIGURE 197**

TRANSLATED

CGGCTCGAGCCGCCCGAAGTGCCCGAGGGGCCGATGGAGCTGGGGAGCCGGCGCTC  
 GGTAGCGCGGCCGGCAAGGCAGGCGCC**ATG**ACCCCTGATTGAAGGGTGGGTATGAGGTGAC  
 CGTCCTTCTCGGTGCTTGCTGCCTCTGGTCTGCCCTGGCTCAACGCACA  
 CCGCTGAGGGCGGGACCCACTGCCAGCCGTAGGGACCCAACGCCATCCCAGCCCAGC  
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGAGGCCAGGGCAGAGACCCCCAGCCT  
 GAGACACAGAGGTCAAGCTGCACAGCCAGGCCAGCACGGGTTCACAGAACACCGCCAG  
 CCCCAGACTCCCCGAGGAGCCCTCGTGTACGGCTGAAATTCTCAATGATTAGCAGAGCAG  
 GTGGCCAGGGCTGGCCCCACGACACCATTGGCTCCTGAAAAGGACCCAGTTCCGGCCG  
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCACGACACCCAGACCCCTGG  
 GCAGCCTTCACCTCCCTCCAACTGCCTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC  
 CCAAATCCCCCTGCCCGCCGGGTCCGAGCCGCCCTCCGGCTGGAAATCGGCAGCCT  
 GCTGCTGCCCTGCTCCTGCTGTTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC  
 CCTTCTTCCCTGACCGCCACTCTGGCCTGCCGGCTTCACCCTGCTCCTCAGTCTCCTG  
 GCCTTGCCATGTACCGCCG**TAG**TGCTCCGCCGGCGCTTGGCAGCGTCGCCGGCCCTCC  
 GGACCTTGCTCCCCCGCCGCCGGAGCTGCTGCCCTGCCAGGCCGCCCTCCGGCCTG  
 CCTCTCCGCTGCCCTGGAGCCCAGCCCTGCCCGCAGAGGACTCCGGACTGGGGAGG  
 CCCCAGCCCTGCGACCGCCGGGCTGGGGCACCTCCGGGCTGCTGAACCTCAGCCGCA  
 CTGGGAGTGGCTCCTCGGGATCTGCTGTCGCTGCCCTGCCGGCAGAGCCG  
 GGCGCCCCGGGGCCGTCTAGTGTCTGCCGGAGGACCCAGCCGCCCTCCAATCCCTGAC  
 AGCTCCTGGCTGAGTTGGGACGCCAGGTGGTGGAGGCTGGTGAAGGGAGCGGGAG  
 GGGCAGAGGAGTTCCCCGGAACCGTGCAGATTAAAGTAACGTGAAGTTAAAAAAAAAA  
 AAAAAAAA

## **FIGURE 198**

MTLIEVGVDENVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS  
EPGPSGLEIGSLLLPLLLLLLWYCQIQYRPFFPLTATLGLAGFTLLSLLAFAMYRP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217

**FIGURE 199**

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG  
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCCTAAGAACCATCAGCCC  
TCAGCTGCACCTCCTCCCTCCAAGGATGACAAAGGCCTACTCATCTATTGGTCAGCAGC  
TTTCTTGCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTGGCCAGGTGCTGCAGC  
GGAGGACTTGGATGGGTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTGTGG  
AAAGCAAGTTAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTGACTATGGCCTC  
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTGCCA  
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTGCAGGCATCCACTGCGAAAAAGGA  
TTGTGTCCGGAGCACGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTAGGCCGG  
CCACTCTCCTACTGGCTGACAGGATGCCGCTGAGATGAAACAGGGTGCAGGTGCACCGTGG  
AGTCATTCCAAGACTCCTGCTCACTCAGGGATTCTCATTCTTCTTCTACTGCCTCCA  
CTTCATGTTATTTCTTCCCTCCCATTACAACAAACTGACCAGAGCCCCAGGAATAAA  
TGGTTTCTTGGCTCCTCCTACTCCCATCTGGACCCAGTCCCTGGTCTGTCTGTTAT  
TTGTAAACTGAGGACCACAATAAGAAATCTTATATTATCG

## **FIGURE 200**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSSENLCHVDCQDLLNPNILLAGIHCAKRIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
```

**Signal peptide:**

amino acids 1-18

## **FIGURE 201**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAAGCCCTGCTTGACTGAGAACCCA  
CCAGCTCATCCAGACACCTCATAGCAACCTATTATAACAAAGGGGAAAGAAAACACCTGAG  
CAGAATGGAATCATTATTTTCCCAGGAGAAAACCGGGTAAAGGGAGGGAAAGCAATT  
AATTGAAAGTCCTGTGAATGGGCTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC  
TTGGGGTGAAGACTTGGGCTCTGTGGTTCTGATTGTAAGTGAAGCAGGTCTGCACACGC  
TGTGCAAATGTCAGGACCAGGTTAAGTGAAGCAGAAAAACTTCCAGGTGGAACAAGCA  
ACCCATGTTCTGCTGCAAGCTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTGAACATGAC  
CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG  
CAGACTCCAGTCCCTCCTGCTGCTCCTGATGCTGGATGCGTCTGATGATGGTGGCGATGT  
TGCACCCCTCCCCACACACCCTGCACAGACTGTACAGGCCAAGGCCAGCAAGCACAGCCCT  
GAAGCAGGTACCGCCTGGACTTTGGGAATCCCAGGATTGGTACTGGAAGCTGAGGATG  
GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCCTTATCTCACTGCAGGGAGGATCAGC  
TGCTGGTGGCCGTGGCCTTACCCCAGGCCAGAAGGAACCAGGCCAGGGCAGGGAGAGGTGG  
AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG  
GGCTGATGAGGACGGGGAGGTGTCGAAGAAGAGGAGTTGACCCGTTCAGCTGGACCCAC  
GTGGCCTCCAGGAGGCACTCAGTGCCTGCATCCCCCTCCAGAGGGCTTGCCAGGTGCGG  
CACCCACTGTGCTGCAGCAGCACCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG  
TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTGACACAGTGC  
CCAGGGCCTCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTAAG  
TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG  
GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACCAGGCCACGGGGATGTGCTGCT  
TCATGGATGCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCCTCTCAGCAGAAATAGCT  
GGTGAAGGAGCCGAGTGGTATCTCCGGTGAAGATGTGATTGACTGGAAGACTTTCCAGTA  
TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCACGGAAAC  
CTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCATAAGCCCCATCAGGAGCCCTGTG  
GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC  
TCTTATGTCGCTGCGAGGTGGTGAACACTGTCTTCAAGGCCCTGGCTCTGTGGT  
GCTCTGTTGAAATCCTCCCTGCTCTGGTAGGACACATCTACCAAAATCAGGATTCCCAT  
TCCCCCTCGACCAGGAGGCCACCCCTGAGGAACAGGGTTCGCATTGCTGAGACCTGGCTGG  
GTCATTCAAAGAAACCTCTACAGCATAGCCAGGGCCTCTCCTGAGCAAGGCTGAGA  
AGCCAGACTGCATGGAACGCTTGCAAGCTGCAAAGGGAGACTGGGTTGCGGACATTCCACTGG  
TTTCTGGCTAATGTCTACCCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTCTCTGGAAA  
GCTCCACAACACTGGACTTGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGG  
GTCCTGGCTTGGCTCTGCAAGTGCACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC  
AGGAAGGAGATTCACTTGGCAGCCCACAGCACCTGTGCTTGCTGCAAGGAGCAGGT  
GATTCTTCAGAACTGCACGGAGGAAGGCCATCCACCCAGCAGCACTGGGACTTCAGG  
AGAATGGGATGATTGTCACATTCTTCTGGAAATGCATGGAAGCTGTTGCAAGAAAAC  
AATAAAGATTGTACCTGCGTCCGTGTGATGGAAAAGGCCGCCAGCAGTGGCATTGACCA  
GATAAATGCTGTGGATGAACGATGAATGTCATGTCAGAAGGAAAAGAGAATTGGC  
AAAATCCAGCTCCAAGTGAACGTAAGAGCTTATATATTGACAGCTGATGACCTTTGTGT  
GTGTGCTCCTGTGTTAGGAGAGAAAAAGCTCATGAAAGAATATAGGAAGTTCTC  
TCACACCTTATTGACTGCTGGCTGCTTA

**FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760  
><subunit 1 of 1, 639 aa, 1 stop  
><MW: 73063, pI: 6.84, NX(S/T): 2  
MLLRKRYRHRPCRLQFLLLLMLGCVLMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG  
ESQDWVLEAEDEGEYESPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR  
RQDKEAPKRDWGADEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP  
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIILVDDLSQQQLKSALSEYVAR  
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP  
VIDVIDWKTFOYYPSKDLQRGVLDWKDFHWEPLPEHVRKALQSPISPPIRSPVVPGEVVAMD  
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIFYQNQDSHSPLDQEATL  
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEPDCMERLQLQRLGCRTFHWFLANVYEL  
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP  
QHLCFAVRQEQLVQNCTEEGLAIHQHQHWDFOENGIVHILSGKCMEAVVQENNKDLYLRPC  
DGKARQQWRFQINAVDER

**Signal peptide:**

amino acids 1-28

## FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGAC**ATGGA**  
 GTCCAGGATGTGGCCTGCGCTGCTGCTGCCCACCTCCTCCCTCTGGCCACTGCTGTTGC  
 TGCCCTCCCACCGCCTGCTCAGGGCTTCTCATCCTCCCTCGAACCCCACCAGCCCCAGCC  
 CGCCCCCGTGTGCCAGGGAGGCCCTCGGCCAACGTCATGTGTGCGTGTGGGAGCGAGC  
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTCGGCAAGTCCTGCCTGGCACTG  
 CACCCCCAGCCACCCATCAGGCTTGGAGGAGGGCCGCCCTCATCCAAATACCCCTGGGCT  
 ATCGTGTGGGTCCACCGTGTCTCGAGAGGATGGAGGGACCCAACTTGCAATCCC  
 ATTTCTGGACTATGGTTGCAGCCCTCATGGGCTCGAACCCCACACCCAACTCAGACT  
 CCATGCGAGGTGATGGAGATGGGTTATCCTGGAGAGGCACCTGCCACCCCTGCGGCCATT  
 CTGTTGGGGCCGTGGGAAGGTGTGGACCCCAAGCTCTATGTCACAATTACCATCTCCAT  
 CATCATTGTTCTCGTGGCCACTGGCATCATCTCAAGTTCTGCTGGGACCGCAGCCAGAAGC  
 GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGGAGAGCCAGCAGCCACTGACA  
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGCCTCGGGGACTCACCTACCCCCACCC  
 TGACCATGAGGAGCCCCGAGGGGACCCCGGCCCTGGGATGCCCAACCCAAAGGGGCTCCAG  
 CCTTCCAGTTGAACCGG**TGA**AGGGCAGGGCAATGGGATGGGAGGGAAAGAGGGAAGGCAAC  
 TTAGGTCTTCAGAGCTGGGTGGGGTGCCTCTGGATGGTAGGTAGTGAGGAGGCAGGCAGTGGC  
 CTCCCACAGCCCTGGCCCTCCAAGGGGCTGGACAGCTCTCTGGGAGGCACCCCTTC  
 CTTCTCCAGTCTCTCAGGATCTGTGCTTATTCTCTGCTGCCATAACTCCAACCTGCCC  
 TCTTGGTTTTCTCATGCCACCTGTCTAAGACAACCTGCCCTTTAACCTTGATTCCC  
 CCTCTTGTCTTGAACCTCCCTCTATTCTGCCCTACCCCTGGTCTCTGACTGTGCCCTT  
 TCCCTCTCCTCTCAGGATTCCCTGGTAATCTGTGATGCCCAATGTTGGGTGCAGCC  
 AACGAGGAGGCCAAGGGGCCGGCACAGCCCCCATCCCACTGAGGGTGGGCAGCTGTGGGA  
 GCTGGGCCACAGGGCTCTGGCTCTGCCCTTGACACCACCCGGAACACTCCCCAGCC  
 CCACGGCAATCCTATCTGCTGCCCTCTGCAGGTGGGGCTCACATATCTGTGACTTCG  
 GGTCCCTGCCCCACCCTTGCACTCACATGAAAGCCTTGACACTCACCTCACCTCAC  
 AGGCCATTGCACACGCTCTGCACCCCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT  
 CATGTTCTCGTCTCACATTGCACCTCTCTTCCACATTCTGTGCTCAGCTCACTCAG  
 TGGTCAGCGTTCTGCACACTTACCTCTCATGTGCTTCCGGCTGATGTTGGTGG  
 TGTGCGGCGTGCTCACTCTCCCTCATGAACACCCACCCACCTGCTTCCGAGGCCCTGC  
 GTGCTGCTCCAGAGGTGGTGGAGGTGAGCTGGGGCTCCTGGGCCCTCATCGTCATGG  
 TCTCGTCCCATTCCACACCATTGTTCTCTGTCTCCCACCTCAAGGATGCCGGCA  
 TCACCCCTGAGGGCTCCCCCTGGGAATGGGGTAGTGAGGCCAGACTCACCCCCAGGCC  
 CTGCTAAATCTGTTCTGACAGATGGGTTTGGGAGGTGAGCTGGGGCTCCTGGGCCCT  
 AGGGACTCCCATTGCCCTTCCCTTCTCACAGTCCCTTGTCTGTCTGCTGGCTG  
 TCTGTGTGTGCCCCATTCTCTGGACTTCAGAGCCCCCTGAGGCCAGTCCTCCCTCCAGCCT  
 CCCTTGGGCCCTCCCTAACCTCACAGGCTGCCAGGGACGGAGTCAGCTGGTTCAAGGCC  
 ATCGGGAGCTGCCTCCAAGTCTACCCCTCCCTGGGACTCCCTCTGTCCCCCTCCTT  
 CCTCCCTCTTCCACTCTTCCCTTGTCTCCCTGCCCTTCCCCCTCCTCAGGTT  
 CCTCCCTCTTCACTGGTTTCCACCTTCCCTCCCTTCTCCCTGGCTCTAGGCT  
 GTGATATATATTTGTATTATCTCTTCTTGTGGTGATCATCTGAATTACTGTG  
 GGATGTAAGTTCAAAATTCAAATAAGCCTTGCAAGATAA

## **FIGURE 204**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRRLGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIIFYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSYPKGDASTGWNSVSRIIEELPK
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

**FIGURE 205**

GTAAACCAGCGCAGTCCTCCGTGCGTCCGCCGCGCTGCCCTCACTCCGGCCAGG**ATGG**  
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGGTCTCCGGGTTCTGGCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCGTGCCACGCTGTGGAACGAGCCGGCGAGCTGCC  
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGAGCCCGTGGACACCGGTCCCC  
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC  
GGCGGGTCTGGCCGCTGGGCCCCGGCGCTATCGCGGCCATCGTATCGCCGCCCTGCTGGCCACCTG  
CGTGGTGCTGGCGCTCGTGGTCGCGCTGAGAAAGTTTCTGCCTCC**TGA**AGCGAATAAA  
GGGGCCGCGCCGGCCGCGCGACTCGGCAAAAAAAAAAAAAA

## **FIGURE 206**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

## **FIGURE 207**

GGCGTGGTGGTGGCGCGCTGAAGGGTGTGGCGAGCAGCGTCGTTGGTGGCCGGCG  
 CGGGCCGGGACGGGCAAT**GG**CCCTGCTGCTGTGCCCTGGTGTGCCTGACGGCGCGCTGGCCA  
 CGGCTGTCTGCACGTGCCACAGCAACTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA  
 ACTTCAAGTCCTGGTGGGTGGCGACATCCCCGTGTCAGGGCGCTGCTACCGACTGGAGC  
 GACGACACGATGAAGGAGCTGCACCTGCCATCCCCGCAAGATCACCCGGGAGAAGCTGGA  
 CCAAGTGGCGACAGCAGTGTACCAAGATGATGGATCAGCTGTACCAAGGGAGATGTACTTCC  
 CCGGGTATTCCCCAACGAGCTGCACAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
 GCCATCATCGAAAGGCACCTGGCACCAAGGCAGCTGGGGAGGAGGGCAGCTCTCAGGGAGGG  
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATACCCCCGGGGACCTCCCCTAAGTAGCCC  
 CCAGAGGCGCTGGAGTGTGCCACCGCCCTCCCTGAAGTTGCTCCATCTCACGCTGGGG  
 GTCAACCTGGGGACCCCTTCCCTCCGGGCATGGACACACATACATGAAAACCAGGCCGCAT  
 CGACTGTCAGCACCGCTGTGGCATCTCCAGTACGAGACCATCTCTGCAACAACTGCACAG  
 ACTCGCACGTCGCCTGCTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT  
 GCCAGGGCCCTACTGTCCTGGGTCCCAGGCTCTCCTGGAGGGGCTCCCCGCCTCCAC  
 CTGGCTGTATCGGGTAGGGCGGGCGTGGTTCAAGGGCGCACCACCTCCAAGCCTGTGT  
 CCCACAGGTCTCGCGCAGTGGAAAGTCAGCTGTCCAGGGCCTCCTGAACACTACATAAAAC  
 TGGCACAAGTAAGTCCCCTCTCAAACCAACACAGGCAGTGTGTATGTGAGCACCTCGT  
 GGTGAGTATGTGTGGGCACAGGCTGGCTCCCTCAGCTCCACGTCCTAGAGGGCTCCGA  
 GGAGGTGGAACCTCAACCCAGCTCGCGAGGAGGCAGCTGCAGTCCTTCTCCCTCAAAG  
 GTCTCCGACCCTCAGCTGGAGGCAGCTTCCTAAAGGGTCCCCATAGGGTCTGGTTCC  
 ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGAGGGTCCCTACGATGGTTAGGGTGCCTCC  
 ATGGAGGGCTGACTGCCACATTGCCTTCAGACAGGACACGAGCATGAGGTAAGGCCGC  
 CCTGACCTGGACTTCAGGGGAGGGTAAAGGGAGAGAGGAGGGGGCTAGGGGGCTCT  
 AGATCAGTGGGGCACTGCAGGTGGGCTCTCCCTACCTGGACACCTGCTGGATGTAC  
 CTCTGCAACCACACCCATGTGGTGGTTCATGAACAGACACCAGCTCTGCCTCTCCTGG  
 CCTGGACACACAGAGCCACCCGGCCTGTGAGTGACCCAGAGAAGGGAGGCCTGGAGA  
 AGGGGTGCTCGTAAGCCAACACCAGCGTGCAGCGCTGCACACCCCTGGACATCCCAGGC  
 ACGAGGGTGTGAGTGTGGCACACATAGGACCAACACGTCCCAGCTGGAGGGAGAGGCCT  
 GGGGCCCCAGGGAGGGAGGCAGGGGTGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
 CCGCAGCCTGGTATGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT  
 TGGAAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGCCTGCCAGGGCAAC  
 GTGGGGCGGAGACTCAGCTGGACAGCCCCTGCCTGTCACTCTGGAGCTGGCTGCTGCTGC  
 CTCAGGACCCCTCTCCGACCCGGACAGAGCTGAGCTGGCCAGGGCAGGAGGGGGAGG  
 GAGGGAAATGGGGTGGCTGTGCGCAGCATCAGCGCCTGGCAGGTCCGAGAGCTGCGGGGA  
 TGTGATTAAAGTCCTGATTTCTC

## **FIGURE 208**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMK
ELHLAIAPAKITREKLDQVATAVYQMMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER
HLAPGSWGGQLSREGPSLAPEGSMPSPRGDLP
```

**Signal peptide:**

amino acids 1-15

## FIGURE 209

AGCAGGGAGCAGGAGAGGGACA**ATG**GAAGCTGCCCGTCCAGGTTCATGTTCCCTCTTATTCT  
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG  
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTGCTGCC  
 ACTGAGGTGGCTGTCATAGGCTTCTTCAGGATTAGAAATACCAGCAGTGCCCATACTCCA  
 TAGCATGGTGCAAAAATTCCCAGGCAGTCATTGGGATCAGCACTGATTCTGAGGTTCTGA  
 CACACTACAACATCACTGGAACACCCTGCCTCTTCGCCTGGTAGACAATGAACAACTG  
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTCTGAGAT  
 CAACAGCCTCCACATGGTACAGAGTACAACCCGTGACTGTGATTGGGTTATTCAACAGCG  
 TAATTCAAGATTCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG  
 CACAGATACCAGAAGGCAGCCAAGCTCTCCAGGGGAAGATTCTCTTATTCTGGTGGACAG  
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTCAAACTAAAGGAGTCTCAACTGCCAG  
 CTTGGCAATTACCAAGACTCTAGATGACGAGTGGATACACTGCCACAGCAGAAGTTCC  
 GTAGAGCATGTGCAAAACTTTGTGATGGATTCTAAGTGGAAAATTGTTGAAAGAAAATCG  
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**TGA**CTTCTCCTTGGAACTACATATGCC  
 AAGTATCTACTTATGCAAAGTAAAAGGCACAACACTCAAATCTCAGAGACACTAAACAAACAG  
 GATCACTAGGCCTGCCAACACACACACACACGACGTGACACACACGCACGCGTGCACAC  
 ACACACGCGCACACACACACACAGAGCTCATTCCCTGTCTAAAATCTCGTTCTC  
 TTCTCCTCTTTAAATTCTATCCTCACTCCCTATCCAATTCCCTTATCGTGCATT  
 CATACTCTGTAAGCCCCTGTAACACACACTAGATCAAGGCTTAAGAGACTCACTGTGATG  
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTGTCATTAATATCAAGT  
 TTGTATACTGCACATGACTTACACACACATAGTTCTGCTCTTTAAGGTTACCTAAGGGT  
 TGAAACTCTACCTCTTCATAAGCACATGTCCGTCTGACTCAGGATCAAAACCAAAGG  
 ATGGTTTAAACACCTTGTGAAATTGTCTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC  
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTGGTTAGCATCTCCAACCTCC  
 TATGTAATCAACAAACCTGCATAATAAAAGGCAATCATGTTATA

## **FIGURE 210**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAAEVAEEVEKSSDGPAAQEPWTLDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGFISTDSEVLTHYNITGNTICLFRVLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMVTEYNPVTIVIGLFNSVIQIHLIMNKAPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

## FIGURE 211

GGAGAGCCGGCTGGACCGGAGTGGGGAGCGCGCGTGGAGGTGCCACCCGGCGGGGTG  
 GCGGAGAGATCAGAACCTCTCCCCAAGCCAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
 GACGCGGCGGCGGGCGGCGACTGCAGTGGCTGGACG**ATG**GCAGCGTCCGCCGGAGCCGGG  
 GCGGTGATTGCAGCCCCAGACAGCCGGCGTGGCTGTGGTGGCTGGCGGGCTTGG  
 GCTCTGACAGCTGGAGTATCAGCCTGGAAGTATACGCCAAAAGAAATCTCGTGGCAA  
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC  
 TCAGTCTCTGGAGCTCCAGCCAGAGGGGCGACACTACTGTGTCGTTTCCACTACTC  
 CCAAGGGCAAGTGTACCTGGAATTATCCACCATTAAAGACAGAACATCAGCTGGCTGGAG  
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTATACACAATGGCACC  
 TATATCTGTGATGTCAAAAACCCTCCTGACATCGTTGTCAGCCTGGACACATTAGGCTCTA  
 TGTGTTAGAAAAAGAGAATTGCCTGTGTTCCAGTTGGTAGTGGTGGCATAGTTACTG  
 CTGTGGCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTCTATAGAAGGAAA  
 AACTCTAACGGATTACACTGGCTGCAGTACATCAGAGAGTTGTCACCAGTTAACGAGGC  
 TCCTCGGAAGTCCCCCTCGACACTGAGGGTCTGTAAAGAGTCTGCCTCTGGATCTCACC  
 AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC  
 AAGTCAGAGTCTGGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAACATCTAGAACATATC  
 CTCAGCAAGAACAAAACAAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT  
 AGCCTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT  
 ACAAAAGGATATGTATAAATATTCTATTAGTCATCCTGATATGAGGAGCCAGTGGTGCATGA  
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTGCTGTTTGTACTTCTTTTC  
 AGGTCATTACAATTGGGAGATTCAGAAACATTCCCTTACCATCATTAGAAATGGTTG  
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTCCAGTAGACATGGCCTTTAATCTAAG  
 GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
 GCATACCCAGGGTGGCCTTACAGTACGTTAGTACCTGCTGCCGCTTTAAAAA  
 AATACCCATTGGCTATGCCACTTGAAAACAATTGAGAAGTTTTGAAGTTTCTCACT  
 AAAATATGGGCAATTGTTAGCCTTACATGTTGTAGACTTACTTAAGTTGCACCCCTG  
 AAATGTGTCATATCAATTCTGGATTCTAAATAGCAAGATTAGCAAAGGATAATGCCGAAG  
 GTCACCTCATTCTGGACACAGTTGGATCAACTGATTAAGTAGAAAATCCAAGCTTGCTT  
 GAGAACTTGTAACGTGGAGAGTAAAAAGTATCGGTTTA

## **FIGURE 212**

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKDASINEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDYTGCSTSESLSPVKQAPRKSPSDTEGLVKSILPSGSHQGPVIYAQLDHSG
GHSDKINKSESVVYADIRKN
```

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

## **FIGURE 213**

CCCGGGCTGTGCAGAGACGCC **ATG**TACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCC  
TCTCGGCCACGGCTGGTCGGGGCCTCGGGCTGGGCTGGGCTGGCGCTGGGGTGAAGC  
TGGCAGGTGGCTGAGGGCGCGGCCCCGGCGCAGTCCCCCGGGCCCCGACCCCTGAGGCG  
TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTGCCCGTGGCTCCGCAGACCCGGC  
GCCGCCCTGCTCCAGGTGCTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA  
TCAAGGATGAGGTGGCGCACCGGCATAGTGGTTGGAGTTCTGTAGATGGAAAAGAAGTC  
TGGTCAGAAGGTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAACCAAGAGACAGT  
TATGCGAATTGCTAGCATCAGAAAAGTCTCACCATGGTGTCTGCCAAATTGTTGGAAAG  
CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCGAATTCCAGAAAAAGAA  
TATGAAGGTGAAAAGGTTCTGTCAACAACAAGATTACTGATTCCCATTAAAGCCTTGAAAGATGA  
TCATTATGAAAAGGACATAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAAGATGA  
TGAAAGAGAATGTTGCATTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTT  
ACTAAATTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGAATTCAAAACCTGGCAAGAA  
AAAGAATGATTTGAACAAGGCGAATTATATTGAGAGAAAAGTTGAAAATTCAATTGAAT  
CCCTAAGATTATTAAAAATGATCCTTGTCTTCAAACCTGGTAGTCAGTTTGATTCA  
ACTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTCAGGATGTAATATTGGA  
CTATATGCAGAAAATATTCCATGACTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
CAGTGATTTACAATAGAGCAAGG **TA**ATGAATACCTCTGCTGTCTAGCTATATCGCATC  
TTAACACTATTATTAAATTAAAAGTCAAATTCTTGTCCATTCAAAATCAACCTGC  
CACATTGGAGCTTCTACATGTCTGTTCTCATCTGAAAGTGAAGGAAGTAAAACA  
TGTTTATAAAGTAAAAAAA

**FIGURE 214**

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522  
><subunit 1 of 1, 373 aa, 1 stop  
><MW: 41221, pI: 8.54, NX(S/T): 0  
MYRLLSAVTARAAPGGLASSCGRRGVHQRAGLPPPLGHGWVGGIIGLGLALGVKLAGGLRG  
AAPAQSPAAPDPEASPLAEPPQEQLAPWSPQTAPPACSRCFARAIESSRDLLHRIKDEVGA  
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLD  
IPVQHYVPEFPEKEYEGEKVSVTLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF  
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESLRLFKN  
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPMVYNRAR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

**FIGURE 215**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACCGTACGTAAGCTCGGAATTGGCTCG  
AGGCTGGTGGAAAGAACGCCGAGATGGCGGGCAGCCAGCGCTGGGCAACCCGGCTGCTCCTGC  
TCTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCAGGGCAGCGGCTGCCGGCCGGACT  
GGTGCAGGAGGGCTGGGCGGAAGGTCGAGAGGGCGAGGCCTGTCACGGTGGCACGGTGGGCTGCT  
GCTGGAGCACTCATTGAGATCGATGACAGTGCCAACTCCGGAAGCAGGGCTCACTGCTCT  
GGAACCAGCAGGATGGTACCTGTCCCTGTCACAGCGGAGCTCAGCGAGGAGGAGCAGGGC  
CGACTCCGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCAAAGGCAGCCGG  
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCCTCCTTGTCCCTGCGTGCTCCCTGG  
TGGAGTCGACCTGTCGGACCAGCTGACCTGCACGTGGATGTGCCGGCAACGTGGTGGC  
GTGTCGGTGGTGACGCACCCCGGGCTGCCGGGCATGAGGTGGAGGACGTGGACCTGGA  
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCAGGCCCTGAGACGGCGG  
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCAGAAGGCAAGAACCCCCAGGAGCAGAAG  
TCCTTCTCGCAAATACTGGATGTACATCATTCCCGTGTCCCTGTTCTCATGATGTCAGG  
AGCGCCAGACACCGGGGCCAGGGTGGGGTGGGGTGGTGGTGGGAGTGGC  
TTTGTGTGTGCCACCCCTCCCTGTAAGTCTATTAAAAACATCGACGATACTGAAATGTG  
TGAACGTTTGAAAAGCTACAGCTTCCAGCAGCCAAAGCAACTGTTGTTGGCAAGACGG  
TCCTGATGTACAAGCTTGATTGAAATTCACTGCTCACTTGATACTGTTATTCA  
GAATGGCTGTCCCCATCCTCATGTTGGCTGTGGAGCTCAGCTGTGTTGGCAGTTAT  
TAAACTGTCCCCAGATCGACACGCAAAAAAAA

## **FIGURE 216**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pi: 5.80, NX(S/T): 1
MAAASAGATRLLLLLMAVAAPSRARGSGCRAFTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPRPGALDGLEA
GGYVSSFVPACSLVESLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQQSFFAKYWMYIIPVVLFLMMMSGAPDTGGQ
GGGGGGGGGGSGLCCVPPSL
```

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

## **FIGURE 217**

GGAGCGCTGCTGGAACCGAGCCGGAGCCGGAGCCACAGCGGGAGGGTGGCTGGCGCCT  
 GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTGTCGTCGGGGCCCACC  
**ATG**CTGGTACTGCCTACCTGCTTTGTAGGCCTCCTGGCCTCCTGCCTGGGCTGGAACCT  
 GTCAAGATGCCGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTCGGTTTC  
 AACTGGACTTCTATCAGGTCTACTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCTAC  
 CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
 TGGCCTGCCTCTACAGTCCTCTTGGCCTAGTGGCCTCCTCCCTGTGGATTGGCTGGTC  
 GCAAGAATTCTTGTGTCCTCTCCCTGACTTACTCACTATGCTGCTAACCAAACCTCT  
 CAAGACTACTTGTGCTGCTAGTGGGCAGCACCTGGTGGCTGTCCACAGCCCTGCTCTT  
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCTGCTGAGT  
 GGATCCCAGCTACCTTGCTCGAGCTGCCTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGCCTGTAGGCCCTTGTGGCTGC  
 CATCCCTCCCTGGCTCTGGCAGGGCCTGGCCCTCGAAACTGGGGGAGAACTATGACC  
 GGCAGCGTGCCTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCTGCGACCGCCGC  
 GTGCTGCTGCTGGCACCATACAAGCTCTATTGAGAGTGTATCTTCATCTTGCTTCCCT  
 CTGGACACCTGTGCTGGACCCACACGGGCCCTCTGGCATTATCTTCTCCAGCTTCATGG  
 CAGCCAGCCTGCTGGCTCTCCCTGTACCGTATGCCACCTCCAAGAGGTACCACCTCAG  
 CCCATGCACCTGCTGTCCTGCTGTGCTCATCGTCGCTCTCTCTTCTATGTTGACTTT  
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTCATAGCCTTCTACTTATTGAGT  
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCTACGGAGAAAGGTGATCCCTGAGACA  
 GAGCAGGCTGGTGTACTCAACTGGTCCGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT  
 CCTTGTCCCTCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTCAGCATTGCTCTG  
 CTGTCATGGTGTGATGGCTCTGCTGGCAGTGGTGGACTCTTCACCGTGGTAAGGCATGATGCT  
 GAGCTGCGGGTACCTCACCTACTGAGGAGGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG  
 GACAAGATAGCTGGGACAGACTCTGAATTCCAGCTATCCGGGATTGTACAGATCTCTGT  
 GACTGACTTTGTGACTGTCCCTGTGGTTCTCCCTGCCATTGCTTGTGTTGGAGGACATGA  
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAGTCCCTCTGTGTTACTCCCATTAGAAA  
 ATAAACACTTTAAATGATCAAAAAAAAAAAA

## **FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLA  
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRC  
LSDRRVLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLY  
RIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSPGQESP  
VESFIAFLLI  
ELACGLYFPSMSFLRRKVI  
PETEQAGV  
LNWFRVPLHSLACLGLLVLHDS  
DRKTGTRNMFS  
ICSAVM  
VMALLAVVGLFT  
VVRHDA  
ELRVPS  
PTEEPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430

## FIGURE 219

GCGACGCGCGGCGGGCGGCGAGAGGAAACGCGGCGCCGGCCGGCCCTGGAG**ATG**  
 GTCCCCGGCGCCGCGGGCTGGTGTCTCGTGTCTGGCTCCCCGCGTGCCTGGCCCA  
 CGGCTTCCGTATCCATGATTATTTGTACTTCAAGTGCTGAGTCCTGGGACATTGATACA  
 TCTTCACAGGCCACACCTGCCAAGGACTTGGTGTATCTTCACACAAGGTATGAGCAGATT  
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCAGGGAACTCAGCAACGGTTCTCATCCA  
 GGACCAAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTCTCCAAGACTCGGGTGGTCC  
 AGGAGCACGGCGGGCGGGCGGTGATCATCTGACAAACGCAGTTGACAATGACAGCTTCTAC  
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTTCTGCTCGG  
 CCGAGACGGCTACATGATCCGCCGCTCTGGAACAGCATGGCTGCCATGGCCATCATT  
 CCATCCCAGTCAATGTCACCAGCATCCCCACCTTGAGCTGCTGCAACCGCCCTGGACCTTC  
**TGGTAGAAGAGTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGAAACCC**  
 AGGAATTTGCTACTTGGATTGGAGATAGCATCTGGGACAAGTGGAGCCAGGTAGAGGA  
 AAAGGGTTGGCGTTGCTAGGCTGAAAGGAAGCCACACCACTGGCCTCCCTCCCCAGG  
 GCCCCCAGGGTGTCTCATGCTACAAGAACAGAGGCAAGAGACAGGCCCTGGCTA  
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGGCCATCTGTGACCTGTACACT  
 CACCTGGCTCCAGCCTCCCCACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG  
 AGTGGTTAAAGAGCTGGTGTGGGACTCAATAAACCTCACTGACTTTAGCAATAAA  
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAA

## **FIGURE 220**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWL PACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFI QDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADI PALFLLGRDGYMIRRSLEQHGLPWAII SIPVNVT SIPTFELLQPPWTFW
```

**Signal peptide:**

amino acids 1-20

**FIGURE 221**

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGCTGGTGGTGA  
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAACCAAGTG  
ACTGGGAAAATGCCCATCCTCCTACTGGCCTACGGCTGTCAGTGCAGACTAGGTGGCAG  
AGGCCAACCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC  
TGAAGACCCAGGGTGCAGCATCTACAAGGACAACAACAAAAGCAGCATACTTGTATGGAT  
TTATCTCAACGCTATTGTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTC  
CGATAAAAAGCTATTACTAWTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

## **FIGURE 222**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVFNVIYLENEDSE
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 223**

CTCGCTTCTCCTCTGGATGGGGGCCAGGGGCCAGGAGAGTATAAAGGCATGTGGAG  
GGTCCCCGGCACACCAGACGCCAGTCACAGGCAGAGCCCTGGG**ATG**CACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTGCCCTGGGGGCCACCTGGCAGGGAAGATGTAT  
GCCCTGGAGGAGGCAAGTATTCAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTCCTGGTAAAAAGTGTCCAGGTGAAACTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTAGGTGGAAATACCCAGGAAGTCACCCCTGCAGCCAGGCGAATAC  
ATCACAAAAGTCTTGTGCCCTCCAAGCTTCCGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTCTATTTGGGAAGCTTGATGCCAGATCCTCTGCCTACCCAGCCAAG  
AGGGGCAGGTGCTGGTGGCATCTATGCCAGTATCAACTCCTGGCATCAAGAGCATTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAACCTCACATACTC  
AGCAAACTCACCGTGGTCGCT**AG**GGTGGGTATGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAAGTGAGTCGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTCTGCAGAAAA

## **FIGURE 224**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLKVSVQVK
LGDSWDVKGALGGNTQEVTIQLPGEYITKVFVAFQAFLRGMVMTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

**Signal peptide:**

amino acids 1-22

## FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTGCCTCTGGCTCCAACGCAGCTCTGGCT  
 GAACTGGGTGCTCATCACGGAACTGCTGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
 CCCCAAATTGCCTGGAAGAATACATCATGTTTCGATAAAGAAGAAATTGTAGGATCCAGTT  
 TTTTTTTAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAGATGCAAAACGTAATAT  
 CCATGAAGATCCTATTACCTAGGAAGATTTGATGTTGCTGCGAATGCGGTGTTGGATT  
 TATTGTTCTGGAGTGTCTGCGTGGCTGCAAAGAATAATGTCAAAATCGGTCCATCT  
 CCCAAGGGTCCAATTTCCTGGTGTCAAGCAGCCCTGACTCACTACAGTGCAGCTG  
 ACAGGGCTGTCACTGCAACTGGCCCTAACGCAAAGCAGCTAACGGACGACCTTGAA  
 CAATACAAAGGATGGTTCAATGTAATTAGGTACTGAGCGGATCAGCTGTAGCACTGGTT  
 ATAGCCCCACTGTTACTGACAATGCTTCTGCCAACGAGGATGCCAACGGCTG  
 TAGGTGTGAAGGCAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCTCAAGTA  
 TATCTGCTGGTTGCTTAGGTTGTCCTCGCTATAACAGCCTCAAAACTTAAGTATAAT  
 CAATTTAAAGGGCTAACACAGTCACCTGGCTACCTGACCATAACCATATCAGCAATAT  
 TGACGAAATGCTTTAATGGAATACGCAGACTCAAAGAGCTGATTCTAGTTCCAATAGAA  
 TCTCCTATTTCTAACACACCTTCAGACCTGTGACAAATTACGGAACTTGGATCTGTCC  
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTGGGGCTTGGGAAGCTGCTGAGTT  
 ACATTTACGGCTAACCTCCCTGAGAACCATCCCTGCGAACATTCCAAGACTGCCGCAACC  
 TGGAACTTTGGACCTGGGATATAACCGGATCCGAAGTTAGCCAGGAATGTCTTGCTGGC  
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAACCTTCAAGCTAACCTGGCCCT  
 TTTCCAAGGTTGGTCAGCCTCAGAACCTTACTGCACTGGAAATAAAACTAGTGTCAAG  
 GACAGACCATGTCCTGGACCTGGAGCTCCTACAAAGGCTTGATTATCAGGCAATGAGATC  
 GAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCTGAACCTGGCAACCTGGGA  
 TTCCAACAAGCTCACATTATTGGTCAGAGATTGGATTCTGGATATCCCTCAATGACA  
 TCAGTCTGCTGGGAATATGGGAATGCAGCAGAAATATTGCTCCCTGTAAACTGGCTG  
 AAAAGTTAAAGGTCTAAGGGAGAAACAAATTATCTGCCCCAAAGAGCTGCAAGG  
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGAAAAGTACTACAGAGAGGT  
 TTGATCTGCCAGGGCTCTCCAAAGCCACGTTAACGCCAACGCTCCCCAGGCCAGCAT  
 GAGAGCAAACCCCTTGGCCCCGACGGTGGAGCCACAGAGCCGCCAGAGACCGATGC  
 TGACGCCGAGCACATCTCTTCCATAAAATCATCGGGCAGCGTGGCGCTTCTGTCCG  
 TGCTCGTCATCCTGCTGGTTATCTACGTGTCACTGGAACCGGTACCCCTGCGAGCATGAAGCAG  
 CTGCAGCAGCGCTCCCTCATGCGAACAGGACAGAAAAAGACAGTCCCTAAAGCAAAT  
 GACTCCCAGCACCCAGGAATTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA  
 TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATGGGCTCCAGGGAGTGTGAGGTA  
**TGA**ACCATTGTGATAAAAGAGCTCTAAAGCTGGGAATAAGTGGTGCTTATTGAACTC  
 TGGTGACTATCAAGGGAACCGCGATGCCCTCCCTCCCTCTCCCTCACTTGGTGG  
 CAAGATCCTCTGCTTGTCCGTTAGTCATTCAATAACTGGTCATTCTCATACATA  
 ATCAACCCATTGAAATTAAATACCAACATCAATGTGAAGCTTGAACCTGGTTAATATAA  
 TACCTATTGTATAAGACCCTTACTGATTCCATTAAATGTCGCATTGTTAAGATAAAACT  
 TCTTCATAGGTAaaaaaaaaaaaa

**FIGURE 226**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTVLLTMSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKELHLEHNQFSKLNLAFLPRLVSLQNLQWNKISVIGQTM
SWTWSSLQRDLGNEIEAFSGPSVFQCVPNLQRLNLDNKLFIGQEILDWSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPLPPTVGATEPGPETDADAEHISFKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT  
 TAAATATGTCAAGATCCAGACTTTCAGTGTACCTCAGCGATCTAACGATAGGGATCTTG  
 TGTTGCCGCTATTCCAGTTGGTCTCGGACCTACCAGCGAAGAAGATGAAATGTGTGT  
 AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGGTTTGG  
 TGGCAGCTCTCTGTGGAGCTGTGGCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCGA  
 ATTGATTCTCACAGGCGCACCATGGCAGTTTGCTGTGGAGACTGGACTCTATTATGG  
 GACAGAAGCAGCTGTGAGTCCAACCTGGAAATTCACCTCAAACACTCAAACCCCTGACCTAT  
 ATCCTGTTCCATGCTCCATGTTGGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
 AAAACAACCTTGATTTAGGTGTGGATTATCAATTAAAGTATTAACGACATCTGTAATTCCA  
 AACATCAAATTAGGAATAGTTATTCAAGTGTGGAAATGTCCAGAGATCTATTCAATA  
 GTCTGAGGAAGGACAATTGACAAAAGAATGGATGTGGAAAAATTGGTACATGGAGATG  
 TTTAAATAGTAAAGTAGCAGGCTTGATGTGCACTGCTGTATCATACTTTATGCTACAC  
 AACCAAATTAATGCTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
 TCCATCACATTAGGACTCCACTGCAGTATACAGCACACCATTCTGCTTAAACTCTTC  
 CTAGCATGGGTCCATAAAATTATAATTAAACAATAGCCCAAGCCGAGAATCCAACAT  
 GTCCAGAACCAAGAACAGAAAGATAGTATTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
 GAAAAGTTGGAGTTGAAGGGTAAAGGATAATGAAGAGGAAAAGGAAAGATTACAAGTCT  
 CAGCAAAACAAGAGGTTTATGCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA  
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGAGAAAAGAAAATTCCC  
 CTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG  
 GCATTTATTGCAGCATCATGCTAACGACCTCGGCATAGGTATCTGTTCCATGAGGACTGC  
 AGAAGTAGCAATGAGACATCTCAAGTGGATTGGCAGTGGCCATCAGCAGGGGACAGA  
 CAAAAACATCCATCACAGATGACATATGATCTCAGCTGACAAATTGTTGAACAAAACAAT  
 AACATCAATAGATATCTAAAAA

## **FIGURE 228**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMCVNNDQHPNGWYIWILLLLV
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAGDLDIYGTEAAVSPPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

## FIGURE 229

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT  
 TTCTCCAGCTCGATCTGGAGGCTGCTCGCCAGTGTGGGACGCAGCTGACGCCGCTTATT  
 GCTCTCGCTCGCGCCCCGGCTCAGAAGCTCCGTGGCGCGCGACCGTGACGAGAAGCCC  
 ACGGCCAGCTCAGTTCTCTACTTTGGGAGAGAGAGAAAAGTCAGATGCCCTTTAAACT  
 CCCTCTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATAACAACCTGCTGAAG  
 ATGAAGAATATACAATATTGAGGATATTTTTCTTTTTCAAGTCTGATTGTGGC  
 TTACCTCAAGTTACCATTTTCAGTCAGTCAGTCTGTTGTTGCTTCAGAA**ATG**TTTTA  
 CAATCTCAAGAAAAATATGTCCCAGAAATTGAGTTACTGTTGCTGTATTGGACTCATT  
 TGGGGATTGATGTTACTGCACTATACTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT  
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACATT  
 GCTGTCCTCTGGATGACATTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT  
 TGTGTGAATGGCTAGCAGCCAACACCACCAATGGTACTAGTGGAAATTGGTGCAGTAA  
 CCACAAATAAAAGAACGAATGTCGGGCAGTATCAGA**TAG**CAGTTGAAAATCACCTTGTGC  
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTATAATTGCTGGCTTAGGAC  
 AGAGCAATACTTACAATAAAAGCTCTACACATTTCAGGAGTATGCTGGATTGAAAC  
 TCTAATTCTGTACATAAAATTAAAGTTATTGTTGCTTCAGGCAAGTCTGTTCAATG  
 CTGTAATGTCCTAAAGAGAATTGGTAACTTGGTGAAGCTGGAGATAGGTGAGT  
 TTTGTATAAAATCTTGTGTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATT  
 ATTTCTATAACACATTATTTAAGTATATAACACGTTTTGGACAAGTGAAGAATGTTAA  
 TCATTCTGTCAATTGTTCTCAATAGATGTAACCTGTTAGACTACGGCTATTGAAAAAATGTG  
 CTTATTGTACTATATTGTTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA  
 TAATGTTGAAATCATGACCCAAAGAACATGATTGACTATCCTCAGAATAACTGA  
 AGGTTAATTATTGTATATTAAAAATTACACTTATAAGAGTATAATCTGAAATGGGTAG  
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTAAATAACAGCATTAAAATAGTT  
 GTAAACTCTAATCTTAACTTATTGAAGAATAAAAGATATTGATGAGAGTAACAATA  
 AAGTATTGATTTTCACATACATGAATGTCATTAAAAGTTAATCCTTGAGTGTCT  
 ATGCTATCAGGAAAGCACATTATTCATATTGGGTTAATTGCTTTATTATATTGGTC  
 TAGGAGGAAGGGACTTGGAGAATGGAACCTTGAGGACTTGTAGCCAGGTGTATAATAAA  
 GGTACTTTGTGCTGCATTAATTGCTGGAAAGTGTAAACATTATATTATAAGAGTATC  
 CTTATGAAATTGTAATTGTATAACAGATGCATTAGATATTCAATTATATAATGCCAC  
 TTAAAATAAGAACATTAAAATATAAACTATGAAGATTGACTATCTTTCAGGAAAAAGCT  
 GTATATAGCACAGGGAACCCATTCTGGGTAAATTCTAGTATAAAACAAATTATACTTTAT  
 TTAAATTCCCTGTAGCAAATCTAATTGCCACATGGTGCCTATATTGATAGTATT  
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTAGATTTAGACTATATAGAATTAGATAT  
 TGTATTGTTGTCATTATAATATGCTACCACATGTAGCAATAATTACAATTGTTATTAAAA  
 TAAATATGTGAAATATTGTTCATGAAAGACAGATTCCAATCTCTCTCTGTAC  
 CTGTCTACCTTATGTGAAGAAATTAAATTATGCCATTGCCAGGT

## **FIGURE 230**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWLGLMLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**FIGURE 231.**

CGCGGCCGGGCGCCGGGCTGAGCGTGCCGAGGCCGCTGTGGCGCAGGCCAGCTTCCAGCCCCCAC  
**CATG**CCGTGGCCCCCTGCTGCTGCTGGCCGTGAGTGGGCCAGACAACCGGCCATGCT  
TCCCCGGGTGCCAATGCGAGGTGGAGACCTCGGCCCTTCGACAGCTCAGCCTGACTCGG  
GTGGATTGTAGCGGCCTGGGCCACATCATGCCGGTGCCTCCATCCCTCTGGACACAGCCA  
CTTGGACCTGTCCCTCAACCAGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCCGGCT  
ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGTCACCAGCATCTCACCCACTGCC  
TTCTCCCAGCCTCGCTACCTGGAGTCGCTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
AGCCGAGAGCTTCACCAAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGG  
AGGTCTCAGTGCTGCCTCACGACGCACAGTCAGGGCCGGCACTACACGTGGACCTCTCC  
CACAAACCTCATCACCGCCTCGTCCCCACCCACGAGGGCCGGCTGCCTGCGCCCACCAT  
TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGGCCC  
TGCCTACCTGAGCCTGGATGGAACCCCTCTAGCTGTATTGGTCCGGTGCCTCGCGGGG  
CTGGGAGGCCTTACACACACTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG  
TGGCTCCGTGAGCTACCGGGCTGCAGGTCTGGACCTGTCGGCAACCCCAAGCTTAAC  
GGCAGGAGCTGAGGTGTTTCAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTCGGGCA  
AACCTGGTCCCCCTGCCTGAGGCCTGCTCCTCACCTCCGGCACTGCAGAGCGTCAGCGT  
GGGCCAGGATGTGGTGCCTGGGAGGGCACCTACCCCGGAGGCCTGGCT  
CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGCCCCACC  
ATCTG**TGA**CAAATGGTGTGGCCAGGGCACATAACAGACTGCTGCTGGCTGCCTCAG  
GTCCCAGTAACCTATGTTCAATGTGCCAACACCAGTGGGAGCCCGAGGCCTATGTGGCA  
GCGTCAACCACAGGAGTTGTGGCCTAGGAGAGGCTTGGACCTGGGAGCCACACCTAGGAGC  
AAAGTCTACCCCTTGTCTACGTTCTCCCCAACCATGAGCAGAGGACTTCGATGCCA  
AACCAAGACTCGGGTCCCCCTGCTTCCCCACTTATCCCCAACGTGCCCTCCCTCAT  
GCCTGGGCCGGCTGACCGCAATGGCAGAGGGTGGTGGACCCCTGTCAGGGCAGA  
GTTCAGGTCACTGGCTGAGTGTCCCCCTGGGCCATGGCCAGTCACTCAGGGCGAGTT  
TCTTTCTAACATAGCCCTTCTTGCCATGAGGCATGAGGCCGCTTCATCCTTTCTAT  
TTCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCCTCATGTGAC  
AGATGGGAAACTGAGGCCTTGAGAAGGAAAAGGCTAATCTAAGTCCCTGCGGGCAGTGGC  
ATGACTGGAGCACAGCCTCTGCCCTCCAGGCCGGACCAATGCACTTCTGTCTCCCTCA  
ATAAGCCCCACCCCTCCCCGCTGGCTCCCCCTGCTGCCCTGCTTCCCCATTAGCACA  
GGAGTAGCAGCAGCAGGACAGGCAAGAGGCCTCACAAAGTGGACTCTGGCCTTGACCAAGCT  
GTGCAGGCATGGCTAACGCACTCTGCCCTCGGAGGCCTCTGGAGCCTAGGGCACATTGGTT  
CCAGCCTAGCCAGTTCTCACCCCTGGTTGGGCTCCCGAGCATCCAGACTGGAAACCTACC  
CATTTCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGAGTCTGGAGCCTCA  
TCTGGCTGGGATCTCCAAGGGCCTCTGGATTAGTCAGTCCCCACTGGCCCTGAGCACGACAGC  
CCTTCTACCCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGACCCATGTCTATGC  
TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCTGGCTGTTCTTAGTCATTCTCATTTA  
TAAAAGTTGTTGCCTTTAACGGAGTGTCACTTCAACCGGCTCCCTACCCCTGCTGGC  
CGGGGATGGAGACATGTCATTGTAAGCAGAAAAAGGTTGCATTGTTCACTTTGTAAT  
ATTGTCCTGGGCTGTGTTGGGGTGTGAGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC  
AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGGCTGCTGCTTCCCCCACCTGCTAGC  
CCATCATCTATCTAACGGCTCTGATTAAATAACACTATAAAAGTTAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 232**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLAVSGAQQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHVDSLHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSIASLQRLPELAPS
GFRELPGLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

## **FIGURE 233**

GATGGCGCAGCCACAGCTCTGTGAGATTGATTCAGTCCCCAGTCCCTGTGGGCTGAGG  
GGACCAAGGGTGAGCTACGTTGGCTTCTGGAAGGGGAGGCTAT**ATG**CGTCAATTCCCCA  
AAACAAGTTGACATTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT  
GTTCCAGGCCTTACCTGCTGGCACTAACGGCGGAGCCAGGATGGGACAGAATAAAGGAGC  
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTGAAATCTCTTCAC  
GGGAGGCTTGGCAGTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCC  
TCTAGTCTTGCCTTCAGCCTCTCTGCTGCGTTATCCTATGGACTCCTCCACTGG  
ACTGAAGACACTCAATTGGAAAGCTGTGATGCCACAAACCTTCAGGAAATACGAAATG  
GATTTCTGAGATAACGGGGCAGTGTGCAAGCAAAGATGGAAACATTGACATCAGAAATCTA  
AGGAGGACTGAGTCTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCCATT  
GCTAAGACTCTATCTGGACAGGGTATTAAAAACTACCAGACCCCTGACCATTACTCTCC  
GGAAGATCAGCAGCCTGCCAATCCTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
GCCCATGACATGCCATTGTGGGAGGAAGCAATGAAGAAATACGCCAGATTCTGAGTCA  
CTTGAAAAGCTGGAACCTCAGGCAGCAGTGTGAAGGCTTGGGGAACTAGACATTCTC  
TGCAATGGATGGAGGAGACAGAA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGT  
CAAGAGCTCCAGTCTCAATACCTGCAGAGGGCATGCCAAACCACTCTTTACT  
GTACTAGTCTGTGCTGGCACAGTGTATCTTATTGCTTACTTGCTTGCATGAT  
TGTCTTATGCATCCCCAATCTAATTGAGACCATACTTGATAAGATTTGTAATATCTT  
TCTGCTATTGGATATATTATTAGTTAATATATTATTATTGCTATTAAATGTATT  
ATTTTTTACTGGACATGAAACTTAAAAAAATCACAGATTATTTATAACCTGACTAG  
AGCAGGTGATGTATTTATACAGTAAAAAAAAACCTGTAAATTCTAGAAGAGTGGCT  
AGGGGGTTATTCATTGTTACTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGA  
TATTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTGATGTGGAATT  
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATTAATTGTT  
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAAGTTTCTTGCATA  
CCAAAAAA

## **FIGURE 234**

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDdrvFKNYQTP
DHYTLRKISSLANSFLTICKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCCTACTGCTGAATGTCCGTCCCAGGAGGAGGGCTTTGCCG  
CTGACCCAGAGATGCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGCGCTACCGTGGC  
CGAGCTAGCAACCTTCCCCTGGATCTCACAAAAACTCGACTCCAAATGCAAGGAGAAGCAG  
CTCTGCTCGGTTGGAGACGGTGCAAGAGAATCTGCCCTATAGGGAATGGTGCACACA  
GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCAT  
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCGAGAGGTTG  
TGTTGGCAAAAGTGAAGATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATG  
GCTGGTGTATTGCCAGTTTAGCCAATCCAACGTGACCTAGTGAAGGTTAGATGCAAAT  
GGAAGGAAAAGGAAACTGGAAGGAAAACCATTGCGATTCGTGGTGTACATCATGCATTG  
CAAAATCTAGCTGAAGGAGGAATACGAGGGCTTGGCAGGCTGGTACCCAATATACAA  
AGAGCAGCACTGGTGAATATGGGAGATTAAACCACTTATGATACTGAAACACTACTGGT  
ATTGAATAACCACTTGAGGACAATATCATGACTCACGGTTATCAAGTTATGTTCTGGAC  
TGGTAGCTTCTATTCTGGAACACCAGCCATGTCATCAAAGCAGAATAATGAATCAACCA  
CGAGATAAACAGGAAGGGACTTTGTATAAATCATCGACTGACTGCTTGATTAGGCTGT  
TCAAGGTGAAGGATTCACTGAGTCTATATAAAGGCTTTACCATCTGGCTGAGAATGACCC  
CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
**TTTAA**

## **FIGURE 236**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLCVVFGKSEDEH
YPLWKSIVGGMMAGVIGQFLANPTDLVKVQMOMEGRKRKLEGKPLRFRGVHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNLNTPLEDNIMTHGLSSLCGLVASILGTP
ADVIKSRMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSLRLMTPWSMVFWLTYEKIREMSGVSPF
```

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## FIGURE 237

CGGACGCGTGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTCCTGCGCGC  
 GCCTGAAGTCGGCGTGGCGTTGAGGAAGCTGGATACAGCATTAAATGAAAAATTATGC  
 TTAAGAAGTAAAAATGGCAGGCTTCAGATAATTTCGTTGCCAGAATGTGAATGTATTG  
 ACTGGAGTGAGAGAAAGAAATGCTGTGCATCTGTTGTCGCAGGTATATTGTTTTACAGGC  
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAACGCCAGAACAGTTGAACCATGCCTT  
 TCACACATGTGGTGTATTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC  
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCTT  
 TTCATTGGTTCATGTTGATGTTGGTCACTTATTGCTTCATGTGGATTCTTTGGTGC  
 ATATGTTACCCAAAATACTGATGTTATCCGGACTAGCTGTGTTTTCAAAATGCACTTA  
 TATTTTTAGCACTCTGATCTACAAATTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC  
 TTCTTAAGTCACATTTCTTTGTTATATTCTGTTAGATAGGTTTTATCTCTCAGT  
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTGTTCTTACATTTTATGTC  
 TGAGTTTGAAATAGTTATGAAATTCTTATTTTCATTGCATAGACTGTTAATATGTA  
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTATTCTGAGATTAGAA  
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTGTCATTTAGAAGTAACCACACTTTGT  
 CTCTCTGGCTGGCACGGTGGCTATGCCTGTAATCCAGCACTTGGGAGGCCAGGG  
 CCGATTGCTTGAGGTCAAGTGTGAGACCAGCCTGGCCAACATGGCAAACCCCCATCTACT  
 AAAAATACAAAATTAGCCAGGCATGGTGGTGGTGCCTGTAATCCCAGCTACCTGGGAGGC  
 TGAGGCAGGAGAATCGCTGAACCCGGGGGCAGAGGTTGCAGTGAGCTGAGTTGCCAC  
 TGCACCTAGCCTGGGGAGAAAGTGAACACTCCCTCTAAAAAAAGACCACTCTCAGTATC  
 TCTGATTTCTGAAGATGTACAAAAAAATAGCTTCATATCTGGAATGAGCACTGAGCCA  
 TAAAAGGTTTCAGCAAGTGTAACTTATTGCTTAAAGGTTTTGGTAAAGA  
 AAAAATATTGTTCTATGTATTGAAGAAGTGTACTTTATATAATGATTAAATGCCCC  
 AAAGGACTAGTTGAAAGCTCTTTAAAAAGAATTCTCTAATATGACTTATGTGAGAA

## **FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVAVAGILFFTGWWIMIDAADVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFGRTEELWT

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

## FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCA  
 CTGGCGCCCCGAAACACTCCGTCTACCCCTGGGCCACTGCATCTAGAGGAGGGCCGTCT  
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGACTGTCAGAAGCTGGCCAGGGTGGT  
 GGTCAAGCTGGGTCAAGGACCTACGGCACCTGCTGGACCACCTCGCCTCTCCATCGAAGCAG  
 GGAAGTGGGAGCCTCGAGCCCTGGGTGGAAGCTGACCCAAGCCACCCCTCACCTGGACAG  
**GATG**AGAGTGTCAAGGTGTGCTCGCCTGGCCCTATCTTGCCATAGTCACGACATGGA  
 TGTTTATTCAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
 GCCTCGCCCACCAAGGAGATCCAGGTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC  
 AGCCAACACTTGCCTTAAATCTGCAGTGGGCCAACGTGTCGTGGCCCTACTATGT  
 GCTTGAAAGACCGCATGATCATGAGTCCTGTGAAAAAACATGTGGCAGAGGCCTAACATC  
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTGACATGTACTCTGG  
 AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCCGGGGGTGCACTGGTGCTGGTGG  
 CCTCCTACGACGATCCAGGGACAAATGAACGATGAAAGCAGGAAACTCTCTGACTTG  
 GGGAGTTCCCTACGAAAACAACGGCTCCGGGACAGCTGGTCTTCATAGGAGCAAAGA  
 CCTCAGGGTAAAAGCCCCTTGAGCAGTTCTAAAGAACAGCCCAGACACAAACAAATACG  
 AGGGATGCCAGAGCTGGAGATGGAGGGCTGCATGCCCGAAGCCATTTCAGGGTGGC  
 TGTGGCTTCCTCAGCCAGGGCCTGAAGAACGCTCTGCCTGACTTAGGAGTCAGAGCCCG  
 GCAGGGCTGAGGAGGAGGAGCAGGGGTGCTGCGTGGAAAGGTGCTGCAGGTCTGCACGC  
 TGTGTCGCGCCTCTCCTCGAAACAGAACCCCTCCACAGCACATCCTACCCGGAAGACC  
 AGCCTCAGAGGGCTTCTGGAACCAGCTGTGTCGTGGAGAGAATGGGTGCTTCGTCAGGG  
 ACTGCTGACGGCTGGCCTGAGGAAGGACAAACTGCCAGACTTGAGCCAAATTAAATTAA  
 TTTTGCTGGTTTGAAAAA

## **FIGURE 240**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLILLALIFAIVTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPKPF
```

**Important features:**

**Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

**FIGURE 241**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGAGATTGTCCTGGGAT  
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA  
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC  
 TCACTCCTCCCTCCCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCC  
 CTGCACCCCTTCCTGGGACACT**ATGTTGTTCTCCGCCCTGCTGGAGGTGATTGGATCC**  
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGCCA  
 GCCTCTTACCCCTGAGTGTGAAACAATGCCAGTCGCCATCGATATTAGACAGACAGTGT  
 GACATTGACCCCTGATTCGCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC  
 CTTTGGACCTGCACAACAATGCCACACAGTCAACTCTCTGCCCTCACCCCTGTATCTG  
 GGTGGACTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGTCAGAAAGGATC  
 CCCAGGGGGTCAGAACACCCAGATCAACAGTGAAGCCACATTGCAGAGCTCCACATTGTAC  
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT  
 GTCCTGGGCATCCTAATTGAGGTGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG  
 TCACCTGCATGAAGTCAGGCATAAAGATCAGAACGACCTCAGTGCCTCCCTCAACCTAACAGAG  
 AGCTGCTCCCCAACAGCTGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTCCCCCT  
 TGCTACCAGAGTGTGCTCTGGACAGTTTTATAGAAGGTCCCAGATTCAATGGAACAGCT  
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAACAGGAGCCCTCTAACGCTCTGGTACAGA  
 ACTACCGAGCCCTCAGCCTCTCAATCAGCGCATGGCTTGCTTCTTCATCCAAGCAGGA  
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTGGTGGCTGCTCTG  
 CCTTCTCCTGGCTTTATTCTATTGCTAGAAAGATTGGAAGAACAGGCTGGAAAACCGAA  
 AGAGTGTGGATGACTTCCCTCATGCCTATCAGGAAGCCTCTAAATGGGTGTAGGATCTG  
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCCTGGACATCTTAGAGAG  
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACACTGCAGAGCCTCAGCCTCTCCAAACATGTA  
 GGAGGAAATGAGGAAATCGCTGTGTTAATGCAGAGANCAAACCTGTTAGTTGCAGGG  
 GAAGTTGGATATAACCCAAAGTCCCTACCCCTCACTTTATGCCCTTCCCTAGATA  
 TACTGCGGGATCTCTCCTAGGATAAAGAGTTGCTGTTGAAGTTGTATTTTGATCAATA  
 TATTGGAAATTAAAGTTCTGACTTT

## **FIGURE 242**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## FIGURE 243

## **FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTIGPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

## **FIGURE 245**

GGAGAGAGGCAGCGCGGGGTGAAAGGCGCATTGATGCAGCCTGCGCAGGCTCGGAGCGCGCG  
GAGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCCTGCCCG  
GCAGCCGGGAGCC**ATG**CGACCCCAGGGCCCCGCCCTCCCCGAGCGGCTCCGCCTCC  
TGCTGCTCCTGCTGCAGCTGCCGCCGCGTCAGCGCCTCTGAGATCCCCAAGGGGAAG  
CAAAGGCGCAGCTCCGGCAGAGGGAGGGTGGACCTGTATAATGAAATGTGCTTACAAGG  
GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG  
GGATCCCAGGTGGGATGGATTCAAAGGAGAAAAGGGGAATGTCAGGGAAAGCTTGAG  
GAGTCCTGGACACCCAACACTACAAGCAGTGTTCATGGAGTTCAATTGAAATTATGGCATAGATCT  
TGGGAAAATTGCGGAGTGTACATTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTGT  
TCAGTGGCTCACTCGGCTAAATGCAGAAATGCATGCTGCAGCGTTGGTATTCACATT  
AATGGAGCTGAATGTTAGGACCTCTTCCATTGAAGCTATAATTATTGGACCAAGGAAG  
CCCTGAAATGAATTCAACAATTAAATTATTCATCGCACTTCTCTGTGGAAGGACTTGTGAAG  
GAATTGGTGTGGATTAGTGGATGTTGCTATCTGGGTGGCAGTTGTCAGATTACCCAAAA  
GGAGATGCTTCACTGGATGGAATTCAAGTTCTCGCATCATTATTGAAGAACTACCAAA**TA**  
**A**ATGCTTAATTTCATTGCTACCTCTTTTTATTATGCCCTGGAATGGTCACTTAAAT  
GACATTTAAATAAGTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTACAGA  
CCAAAGTGTGATTCACACTGTTAAATCTAGCATTATTCAATTGCTCAATCAAAAGT  
GGTTCAATATTTTTAGTTGGTTAGAATACTTCTTCAGTCACATTCTCAACCTA  
TAATTGGAATATTGTTGTGGCTTTGTTCTCTAGTATAGCATTAAATTTAAAAAAATA  
TAAAAGCTACCAATCTTGTACAATTGTAATGTTAAGAATTTCATCTGTTAAAT  
AAAAATTATTCACCAACA

## **FIGURE 246**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217